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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-22

Perfect score: 11

Sequence: 1 ARKS RD MTAIK 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	11	100.0	11	3	AAY88550	Aay88550 NCAM Ig1
2	11	100.0	11	5	ABG69350	Abg69350 Human neu
3	4	36.4	11	2	AAR28088	Aar28088 Cell-to-c
4	4	36.4	11	2	AAR37430	Aar37430 Promega p
5	4	36.4	11	2	AAR83762	Aar83762 NGF deriv
6	4	36.4	11	2	AAW09653	Aaw09653 Labelled
7	4	36.4	11	2	AAY31014	Aay31014 Non-cross
8	4	36.4	11	5	AAU78981	Aau78981 Histone H
9	4	36.4	11	5	AAU78982	Aau78982 Histone H

10	4	36.4	11	5	AAO21655	Aao21655 Histone a
11	4	36.4	11	5	ABG71544	Abg71544 Acetyllys
12	4	36.4	11	5	ABG71541	Abg71541 Acetyllys
13	3	27.3	11	1	AAP82047	Aap82047 "Peptide
14	3	27.3	11	1	AAP91264	Aap91264 Tissue pl
15	3	27.3	11	2	AAR06754	Aar06754 Tumour ne
16	3	27.3	11	2	AAR07719	Aar07719 Peptide f
17	3	27.3	11	2	AAR31358	Aar31358 Antimicro
18	3	27.3	11	2	AAR32352	Aar32352 Human Fac
19	3	27.3	11	2	AAR43465	Aar43465 Ro/SSA ep
20	3	27.3	11	2	AAR45170	Aar45170 Listeria
21	3	27.3	11	2	AAR70606	Aar70606 HIV(B35)A
22	3	27.3	11	2	AAR79902	Aar79902 Human FK-
23	3	27.3	11	2	AAR64598	Aar64598 RF-1 pept
24	3	27.3	11	2	AAR96813	Aar96813 Human lam
25	3	27.3	11	2	AAR96812	Aar96812 N.gonorrh
26	3	27.3	11	2	AAR96834	Aar96834 N.gonorrh
27	3	27.3	11	2	AAW15309	Aaw15309 78 kDa gl
28	3	27.3	11	2	AAW32498	Aaw32498 Helicosta
29	3	27.3	11	2	AAW41012	Aaw41012 Anti-glut
30	3	27.3	11	2	AAW40399	Aaw40399 NNOS bind
31	3	27.3	11	2	AAW62282	Aaw62282 Synthetic
32	3	27.3	11	2	AAW41078	Aaw41078 ADPHK pro
33	3	27.3	11	2	AAW46000	Aaw46000 Peptide #
34	3	27.3	11	2	AAY20426	Aay20426 Human mic
35	3	27.3	11	2	AAW61162	Aaw61162 IgE deriv
36	3	27.3	11	2	AAY03092	Aay03092 New nocic
37	3	27.3	11	2	AAY29752	Aay29752 Modified
38	3	27.3	11	2	AAY47615	Aay47615 Immunogen
39	3	27.3	11	2	AAW74077	Aaw74077 Fragment
40	3	27.3	11	2	AAW74135	Aaw74135 GI transp
41	3	27.3	11	2	AAW97473	Aaw97473 Antigenic
42	3	27.3	11	2	AAW97472	Aaw97472 Antigenic
43	3	27.3	11	2	AAW97476	Aaw97476 Antigenic
44	3	27.3	11	2	AAW97477	Aaw97477 Antigenic
45	3	27.3	11	2	AAW97474	Aaw97474 Antigenic
46	3	27.3	11	2	AAW97475	Aaw97475 Antigenic
47	3	27.3	11	2	AAY02916	Aay02916 Fragment
48	3	27.3	11	3	AAY89315	Aay89315 Core poly
49	3	27.3	11	3	AAY81922	Aay81922 Asparagin
50	3	27.3	11	3	AAY81923	Aay81923 Asparagin
51	3	27.3	11	3	AAY81915	Aay81915 Asparagin
52	3	27.3	11	3	AAY81924	Aay81924 Asparagin
53	3	27.3	11	3	AAY81916	Aay81916 Asparagin
54	3	27.3	11	3	AAY81919	Aay81919 Asparagin
55	3	27.3	11	3	AAY81918	Aay81918 Asparagin
56	3	27.3	11	3	AAY81920	Aay81920 Asparagin
57	3	27.3	11	3	AAY81917	Aay81917 Asparagin
58	3	27.3	11	3	AAY81921	Aay81921 Asparagin
59	3	27.3	11	3	AAB16453	Aab16453 Linear pe
60	3	27.3	11	3	AAV88542	Aay88542 NCAM Igl
61	3	27.3	11	3	AAV88549	Aay88549 NCAM Igl
62	3	27.3	11	3	AAB10140	Aab10140 Insertion
63	3	27.3	11	3	AAV93544	Aay93544 Amino aci
64	3	27.3	11	3	AAB09423	Aab09423 Hepatitis
65	3	27.3	11	3	AAV81393	Aay81393 PKC-alpha
66	3	27.3	11	3	AAV54479	Aay54479 Peptide u

67	3	27.3	11	3	AAB29416	Aab29416 Synthetic
68	3	27.3	11	3	AAB26504	Aab26504 Human IgE
69	3	27.3	11	3	AAB08569	Aab08569 Peptide i
70	3	27.3	11	3	AAB08606	Aab08606 Peptide i
71	3	27.3	11	4	AAG65304	Aag65304 Anti-IL-1
72	3	27.3	11	4	AAB55201	Aab55201 Anti-RSV
73	3	27.3	11	4	AAE05275	Aae05275 Human imm
74	3	27.3	11	4	AAG99815	Aag99815 ERA bindi
75	3	27.3	11	4	ABB59308	Abb59308 Drosophil
76	3	27.3	11	4	AAB51034	Aab51034 IgE pepti
77	3	27.3	11	4	AAU16831	Aau16831 Peptide P
78	3	27.3	11	4	AAG62970	Aag62970 Complemen
79	3	27.3	11	4	AAG62982	Aag62982 Complemen
80	3	27.3	11	4	AAG62974	Aag62974 Complemen
81	3	27.3	11	4	AAG62998	Aag62998 Complemen
82	3	27.3	11	4	AAG62984	Aag62984 Complemen
83	3	27.3	11	4	AAG62991	Aag62991 Complemen
84	3	27.3	11	4	AAG62972	Aag62972 Complemen
85	3	27.3	11	4	AAG62976	Aag62976 Complemen
86	3	27.3	11	4	AAG62980	Aag62980 Complemen
87	3	27.3	11	4	AAE05944	Aae05944 Basic ami
88	3	27.3	11	4	AAE05945	Aae05945 Basic ami
89	3	27.3	11	4	AAE12050	Aae12050 Humanised
90	3	27.3	11	4	AAB82287	Aab82287 Phosphory
91	3	27.3	11	4	AAB72872	Aab72872 Human p53
92	3	27.3	11	4	AAB35187	Aab35187 Human Tra
93	3	27.3	11	4	ABB00723	Abb00723 Viral DP1
94	3	27.3	11	4	AAB88242	Aab88242 Hsp-65 pe
95	3	27.3	11	4	AAB88274	Aab88274 Hsp-65 pe
96	3	27.3	11	4	ABP22484	Abp22484 HIV A11 m
97	3	27.3	11	4	ABP23325	Abp23325 HIV A11 m
98	3	27.3	11	4	ABP12972	Abp12972 HIV A02 s
99	3	27.3	11	4	ABP20894	Abp20894 HIV A03 m
100	3	27.3	11	4	ABP22986	Abp22986 HIV A11 m

ALIGNMENTS

RESULT 1
 AAY88550
 ID AAY88550 standard; peptide; 11 AA.
 XX
 AC AAY88550;
 XX
 DT 07-AUG-2000 (first entry)
 XX
 DE NCAM Ig1 binding peptide #22.
 XX
 KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.
 XX
 OS Synthetic.
 XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Example 4; Page 25; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS RDM TAIK 11
||||| |||||
Db 1 ARKS RDM TAIK 11

RESULT 2

ABG69350

ID ABG69350 standard; peptide; 11 AA.

XX

AC ABG69350;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #22.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
KW postischaemic damage; multiinfarct dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
KW Alzheimer's disease; Parkinson's disease;
KW Huntington's disease. atrophic muscle disorder; gonad degeneration;
KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
CC impaired myelination of nerve fibres, postischaemic damage, e.g.
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
CC degeneration associated with diabetes mellitus, neuro-muscular
CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
CC Huntington's disease. The medicament is for the treatment of diseases or
CC conditions of the muscles including conditions with impaired function of
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
CC disorders, and for the treatment of diseases of conditions of various
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
CC ABG69352 represent human NCAM peptides of the invention
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS RD MTA I K 11
| | | | | | | | | | | |
Db 1 ARKS RD MTA I K 11

RESULT 3

AAR28088

ID AAR28088 standard; protein; 11 AA.

XX

AC AAR28088;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (13).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 6..11

FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val
FT sequence (see AAR28087)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Houghten RA;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.
XX
PS Disclosure; Page 37-38; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28087-
CC 88, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
||||
Db 5 RKS 8

RESULT 4
AAR37430
ID AAR37430 standard; peptide; 11 AA.
XX
AC AAR37430;
XX
DT 25-MAR-2003 (revised)
DT 08-SEP-1993 (first entry)
XX
DE Promega peptide 5.
XX
KW Modified peptide substrate; non-radioactive; detection; dansyl;
KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;
KW protein kinases; proteases.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers.
FT Modified-site 1
FT /note= "detection tag= lissamine, Rhodamine"
XX
PN WO9310461-A1.
XX
PD 27-MAY-1993.
XX
PF 12-NOV-1992; 92WO-US009595.
XX

PR 12-NOV-1991; 91US-00791928.

XX
PA (PROM-) PROMEGA CORP.

XX
PI Shultz JW, White DH;
XX
DR WPI; 1993-182698/22.

XX
PT Quantitating presence or activity of enzyme - by incubating with modified peptide substrate and measuring the modified peptide prod.

XX
PS Claim 24; Page 27; 103pp; English.

XX
CC Promega peptide 5 is tagged with dansyl at residue 1 and may be used in a novel non-radioactive method of quantitating the presence or activity of an enzyme. The method can be used for rapid, specific and highly sensitive detection of enzymes such as protein kinases, phosphatases and proteases, esp. in this case protein kinase C. They can be used to study enzyme function in metabolism and in diagnosis of disease. They also allow quantitative determ. of the enzyme's activity. See also AAR37426-36. (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
|||
Db 5 RKS 8

RESULT 5

AAR83762

ID AAR83762 standard; peptide; 11 AA.

XX
AC AAR83762;

XX
DT 18-MAR-1996 (first entry)

XX
DE NGF derived structural analog C(29-35deltaD30A).

XX
KW Neurotrophin receptor; structural analog; nerve growth factor; beta turn; reverse turn; cyclic; tracer; uncharged; hydropathic; inhibition; neurite outgrowth; central nervous system; peripheral nervous system; tumour; neuroma; hormone-receptor interaction site; immunisation; receptor domain-function correlation.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "contains Fmoc protective group"
FT Misc-difference 1
FT /note= "any uncharged or hydropathic amino acid"
FT Misc-difference 11

FT /note= "any uncharged or hydrophobic amino acid"
XX
PN WO9521193-A1.
XX
PD 10-AUG-1995.
XX
PF 07-FEB-1995; 95WO-CA000059.
XX
PR 07-FEB-1994; 94GB-00002331.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Saragovi UH, Lesauteur L, Cuello AC;
XX
DR WPI; 1995-283731/37.
XX
PT New cyclic peptide(s) which bind to neurotrophin receptor and mimic or
PT inhibit neurotrophin activity - useful e.g. for inhibiting neurite
PT outgrowth or treating nervous system disease, tumours, etc.
XX
PS Claim 9; Page 32; 42pp; English.
XX
CC The peptides AAR83760-80 are examples of peptides that bind to the
CC neurotrophin receptor under physiological conditions in vivo or in vitro.
CC The peptides are structural analogs of nerve growth factor (NGF) and
CC contain at least one beta turn (from region 28-36, 43-49 or 91-98) or 3
CC consecutive reverse turns (from region 59-65). The peptides may be
CC cyclised by oxidn. of Cys or other cyclisation procedure and may be
CC linked to a tracer e.g. a metal chelate or radionuclide. The peptides may
CC contain uncharged or hydrophobic amino acids at the N- and C-termini,
CC which are optionally protected by an Fmoc or acetyl protecting group. The
CC peptides are useful for inhibition of neurotrophin, esp. for inhibiting
CC neurite outgrowth, treating central or peripheral nervous system disease,
CC tumours and neuromas, for mapping hormone-receptor interaction sites and
CC receptor domain-function correlation and for immunisation. This peptide
CC is derived from residues 29-35 with a substitution of residue 30 Asp for
CC Ala, and contains a beta turn
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAIK 11
||||
Db 3 TAIK 6

RESULT 6
AAW09653
ID AAW09653 standard; peptide; 11 AA.
XX
AC AAW09653;
XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1997 (first entry)

XX
DE Labelled peptide substrate used in enzyme activity assay.
XX
KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;
KW non-radioactive; electrophoretic separation; protein kinase; protease;
KW phosphatase.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "labelled with rhodamine B detection tag"
XX
PN US5580747-A.
XX
PD 03-DEC-1996.
XX
PF 21-JAN-1994; 94US-00185448.
XX
PR 12-NOV-1991; 91US-00791928.
XX
PA (PROM-) PROMEGA CORP.
XX
PI White DH, Shultz JW;
XX
DR WPI; 1997-033568/03.
XX
PT Non:radioactive assay for measuring enzyme activity - involving
PT electrophoretic sepn. of labelled cleavage prod. from labelled peptide
PT substrate.
XX
PS Claim 5; Col 39-40; 35pp; English.
XX
CC AAW09653 is a peptide substrate used in a non-radioactive assay for
CC measuring enzyme activity. The assay comprises incubating the enzyme with
CC the labelled peptide substrate to form a labelled peptide product;
CC separating the product from the substrate by agarose gel electrophoresis
CC and measuring the amount of product by detecting the label by
CC fluorescence or chemiluminescence. The assay can be performed rapidly and
CC with great sensitivity. This peptide is especially for determining
CC protein kinase C activity, e.g. to study its function in metabolism or to
CC screen for potential inhibitors. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKSR 5
Db 5 RKSR 8

RESULT 7
AAY31014

ID AAY31014 standard; peptide; 11 AA.
XX
AC AAY31014;
XX
DT 21-OCT-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 63.
XX
KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PF 12-NOV-1996; 96US-00747137.
XX
PR 15-JAN-1991; 91US-00641720.
PR 13-OCT-1992; 92US-00959560.
PR 01-JUN-1993; 93US-00069831.
PR 14-MAR-1994; 94US-00212546.
XX
PA (HEMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI; 1999-508153/42.
XX
PT Non-crosslinked protein particles for therapeutic and diagnostic use.
XX
PS Example 22; Col 77-78; 65pp; English.
XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
CC stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30952-Y31135 represent peptides used in the method of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS R 5
||||

RESULT 8

AAU78981

ID AAU78981 standard; peptide; 11 AA.

XX

AC AAU78981;

XX

DT 18-JUN-2002 (first entry)

XX

DE Histone H3 antigenic fragment #5.

XX

KW Histone; antibody; antigen; methyllysine; gene activation;
KW gene repression; heterochromatin; euchromatin; histone methylation;
KW genetic imprinting; gene silencing.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Modified-site 5
FT /note= "Lys is methylated"

XX

PN WO200218418-A1.

XX

PD 07-MAR-2002.

XX

PF 23-AUG-2001; 2001WO-US026283.

XX

PR 25-AUG-2000; 2000US-0227767P.

PR 03-JUL-2001; 2001US-0302747P.

XX

PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX

PI Allis CD, Strahl BD;

XX

DR WPI; 2002-315534/35.

XX

PT New methyllysine-specific antibodies, useful for as diagnostic or
PT screening tools, as well as in identifying regions of heterochromatin or
PT euchromatin.

XX

PS Claim 1; Page 9; 60pp; English.

XX

CC This invention relates to novel methyllysine histone antibodies which
CC specifically bind to histones H3 and H4. The present invention is
CC directed to post translational modifications of histones, in particular
CC the methylation of lysine residues. Methylation of histones has been
CC shown to be important for gene activation and repression. The antibodies
CC are useful in identifying regions of heterochromatin or euchromatin. The
CC antibodies are also useful as diagnostic or screening tools. The
CC antibodies may also be used to analyse chromosomes for regions of
CC transcriptional activity according to differential methylation and also
CC in studies of genetic imprinting and gene silencing. The antibodies may
CC also be useful for studying diseases linked to imprinting such as Prader-
CC Willi syndrome or Angelman syndrome. The present sequence represents the
CC histone antigenic fragment #5 specific for the N terminal of histone H3

CC used to generate anti histone antibodies of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
Db 3 ARKS 6

RESULT 9
AAU78982
ID AAU78982 standard; peptide; 11 AA.
XX
AC AAU78982;
XX
DT 18-JUN-2002 (first entry)
XX
DE Histone H3 antigenic fragment #6.
XX
KW Histone; antibody; antigen; methyllysine; gene activation;
KW gene repression; heterochromatin; euchromatin; histone methylation;
KW genetic imprinting; gene silencing.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5
FT /note= "Lys is methylated"
XX
PN WO200218418-A1.
XX
PD 07-MAR-2002.
XX
PF 23-AUG-2001; 2001WO-US026283.
XX
PR 25-AUG-2000; 2000US-0227767P.
PR 03-JUL-2001; 2001US-0302747P.
XX
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
XX
PI Allis CD, Strahl BD;
XX
DR WPI; 2002-315534/35.
XX
PT New methyllysine-specific antibodies, useful for as diagnostic or
PT screening tools, as well as in identifying regions of heterochromatin or
PT euchromatin.
XX
PS Claim 1; Page 9; 60pp; English.
XX
CC This invention relates to novel methyllysine histone antibodies which
CC specifically bind to histones H3 and H4. The present invention is
CC directed to post translational modifications of histones, in particular

CC the methylation of lysine residues. Methylation of histones has been
CC shown to be important for gene activation and repression. The antibodies
CC are useful in identifying regions of heterochromatin or euchromatin. The
CC antibodies are also useful as diagnostic or screening tools. The
CC antibodies may also be used to analyse chromosomes for regions of
CC transcriptional activity according to differential methylation and also
CC in studies of genetic imprinting and gene silencing. The antibodies may
CC also be useful for studying diseases linked to imprinting such as Prader-
CC Willi syndrome or Angelman syndrome. The present sequence represents the
CC histone antigenic fragment #6 specific for the N terminal of histone H3
CC used to generate anti histone antibodies of the invention
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
||||
Db 3 ARKS 6

RESULT 10

AAO21655

ID AAO21655 standard; peptide; 11 AA.

XX AC AAO21655;

XX DT 05-SEP-2002 (first entry)

XX DE Histone acetyltransferase inhibitor related peptide-alternative SEQ ID 7.

XX KW Cytostatic; amide derivative; coenzyme A; CoA; acetyltransferase; cancer;
KW gene therapy; enzyme inhibitor.

XX OS Unidentified.

XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "This residue is acetylated"

XX PN US6369030-B1.

XX PD 09-APR-2002.

XX PF 29-NOV-1999; 99US-00451034.

XX PR 29-NOV-1999; 99US-00451034.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PI Cole PA, Soccio RE, Lau OD, Khalil EM, Kundu TK, Roeder RG;

XX DR WPI; 2002-506396/54.

XX PT New amide derivatives comprising coenzyme A are histone acetyltransferase

PT inhibitors useful in e.g. the treatment of cancers and gene therapy.

XX

PS Claim 2; Col 20; 20pp; English.

XX

CC The invention relates to novel amide derivatives comprising coenzyme A (CoA). The amide derivatives of the invention can be used for inhibiting acetyltransferase in diseased cells and treating e.g. cancer, and also for use in gene therapy. This sequence represents an alternative version of peptide SEQ ID No7, which is part of a synthetic molecule that acts as an enzyme inhibitor relating to the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
|||

Db 6 ARKS 9

RESULT 11

ABG71544

ID ABG71544 standard; peptide; 11 AA.

XX

AC ABG71544;

XX

DT 31-DEC-2002 (first entry)

XX

DE Acetyllysine-containing peptide H3-23-TKA used in ELISA assay.

XX

KW Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine; functional analysis; acetyllysine-containing protein; pathosis; acetylated protein; disease diagnosis; histone acetylation; mAb; antibody-producing immortalised cell.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Modified by acetyl (Ac) group"

XX

PN WO200274962-A1.

XX

PD 26-SEP-2002.

XX

PF 13-MAR-2002; 2002WO-JP002330.

XX

PR 15-MAR-2001; 2001JP-00074263.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA (NIHA) JAPAN ENERGY CORP.

XX

PI Komatsu Y, Yoshida M;

XX

DR WPI; 2002-750555/81.

XX
PT Production of anti-acetyllysine monoclonal antibody capable of
PT recognizing N approximatelyi-acetyllysine regardless of types of adjacent
PT amino acids, useful in e.g. disease diagnosis and searching for novel
PT acetyllysine-containing proteins.
XX
PS Example 1; Page 7; 45pp; Japanese.
XX
CC The present invention relates to a mouse anti-acetyllysine monoclonal
CC antibody (mAb) capable of recognising N epsilon-acetyllysine, and a
CC method for producing the monoclonal antibody. The produced antibody is
CC useful in searching for and functional analysis of novel acetyllysine-
CC containing proteins particularly in studying pathosis due to acetylated
CC proteins, disease diagnosis, facilitating detection of variation in
CC acetylation levels of histone influenced by various stimulations during
CC Western blotting, analysis of the variable region in the DNA sequence of
CC an antibody gene of an antibody-producing immortalised cell, and judging
CC the degree of homology specific to the sequence during the protein
CC translation. The monoclonal antibody of the invention is capable of
CC recognising N epsilon-acetyllysine regardless of the type of adjacent
CC amino acids and accepting adjacent amino acids over a broad range.
CC ABG71537-ABG71550 represent acetyllysine-containing peptides used for the
CC comparison of reactivities in enzyme linked immunosorbent assay (ELISA)
CC tests with mouse anti-acetyllysine monoclonal antibodies of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
 ||||
Db 6 ARKS 9

RESULT 12
ABG71541
ID ABG71541 standard; peptide; 11 AA.
XX
AC ABG71541;
XX
DT 31-DEC-2002 (first entry)
XX
DE Acetyllysine-containing peptide H3-9-RKS used in ELISA assay.
XX
KW Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine;
KW functional analysis; acetyllysine-containing protein; pathosis;
KW acetylated protein; disease diagnosis; histone acetylation; mAb;
KW antibody-producing immortalised cell.
XX
OS Unidentified.

XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Modified by acetyl (Ac) group"
XX

PN WO200274962-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002330.
XX
PR 15-MAR-2001; 2001JP-00074263.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (NIHA) JAPAN ENERGY CORP.
XX
PI Komatsu Y, Yoshida M;
XX
DR WPI; 2002-750555/81.
XX
PT Production of anti-acetyllysine monoclonal antibody capable of
PT recognizing N approximatelyi-acetyllysine regardless of types of adjacent
PT amino acids, useful in e.g. disease diagnosis and searching for novel
PT acetyllysine-containing proteins.
XX
PS Example 1; Page 7; 45pp; Japanese.
XX
CC The present invention relates to a mouse anti-acetyllysine monoclonal
CC antibody (mAb) capable of recognising N epsilon-acetyllysine, and a
CC method for producing the monoclonal antibody. The produced antibody is
CC useful in searching for and functional analysis of novel acetyllysine-
CC containing proteins particularly in studying pathosis due to acetylated
CC proteins, disease diagnosis, facilitating detection of variation in
CC acetylation levels of histone influenced by various stimulations during
CC Western blotting, analysis of the variable region in the DNA sequence of
CC an antibody gene of an antibody-producing immortalised cell, and judging
CC the degree of homology specific to the sequence during the protein
CC translation. The monoclonal antibody of the invention is capable of
CC recognising N epsilon-acetyllysine regardless of the type of adjacent
CC amino acids and accepting adjacent amino acids over a broad range.
CC ABG71537-ABG71550 represent acetyllysine-containing peptides used for the
CC comparison of reactivities in enzyme linked immunosorbent assay (ELISA)
CC tests with mouse anti-acetyllysine monoclonal antibodies of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
|||
Db 2 ARKS 5

RESULT 13
AAP82047
ID AAP82047 standard; peptide; 11 AA.
XX
AC AAP82047;
XX
DT 19-OCT-1990 (first entry)

XX
DE "Peptide 2" consisting of residues Arg15 to Arg25 of amyloid A protein.
XX
KW Amyloid A protein; secondary amyloidosis; anti-amyloid A antibody.
XX
OS Synthetic.
XX
PN JP63044895-A.
XX
PD 25-FEB-1988.
XX
PF 13-AUG-1986; 86JP-00189810.
XX
PR 13-AUG-1986; 86JP-00189810.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
DR WPI; 1988-094820/14.
XX
PT Anti-amyloid-A protein monoclonal antibody - used esp. for detection of
PT sec. amyloidosis.
XX
PS Claim 2; Page 649; 6pp; Japanese.
XX
CC An antibody capable of recognising Amyloid A and peptide 3 (His37 to
CC Arg47) derived from Amyloid A, but which does not react with other
CC specified peptides (including peptide 2) is useful for detection of
CC secondary amyloidosis. See also AAP82045-6 and AAP82048-9
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RDM 7
|||
Db 1 RDM 3

RESULT 14
AAP91264
ID AAP91264 standard; peptide; 11 AA.
XX
AC AAP91264;
XX
DT 25-MAR-2003 (revised)
DT 20-DEC-1989 (first entry)
XX
DE Tissue plasminogen activator mutant EGAV (V51R: N451Q).
XX
KW Tissue plasminogen activator; mutant; fibrinolysis; EGAV (V51R: N451Q).
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7

XX
PN WO8907146-A.
XX
PD 10-AUG-1989.
XX
PF 03-FEB-1989; 89WO-US000465.
XX
PR 05-FEB-1988; 88US-00152692.
XX
PA (INTE-) INTEG GENETICS INC.
XX
PI Markland W, Livingston DJ;
XX
DR WPI; 1989-249015/34.
XX
PT Rearranged tissue plasminogen activators - prep'd. by altering the DNA
PT sequence to introduce Avr II, Nhe I, Spe I or Xba I cleavage sites.
XX
PS Disclosure; Page 36; 77pp; English.
XX
CC The peptide is encoded by AAN90545. The peptide has tPA activity, with
CC extended in vivo half life. Spacing between tPA domains is increased, to
CC increase rate of fibrinolysis or the resistance to inhibition by
CC endogenous tPA inhibitors present in human plasma. The peptide is used
CC for thrombolysis in the treatment of myocardial infarction, pulmonary
CC embolism, deep vein thrombosis and stroke. See also AAP91265-84. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 7 RKS 9

RESULT 15
AAR06754
ID AAR06754 standard; protein; 11 AA.
XX
AC AAR06754;
XX
DT 25-MAR-2003 (revised)
DT 23-OCT-1990 (first entry)
XX
DE Tumour necrosis factor derived peptide.
XX
KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;
KW infection; inflammation; transplant rejection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5. .5

FT /label= K, Q, R
XX
PN DE3841753-A.
XX
PD 13-JUN-1990.
XX
PF 12-DEC-1988; 88DE-03841753.
XX
PR 12-DEC-1988; 88DE-03841753.
XX
PA (BADI) BASF AG.
PA (BOEH/) BOEHM H J.
XX
PI Boehm HJ, Daum L, Schmied B, Walker N, Zechel JC, Haupt A;
XX
DR WPI; 1990-186573/25.
XX
PT New tumour necrosis factor derived peptide(s) - for treating or
PT preventing neoplastic and auto-immune disease, infection, inflammation
PT and transplant rejection.
XX
PS Example 67; Page 11; 15pp; German.
XX
CC To residue F1 is attached Ac and to residue A11 NH2. A3 and K9 form
CC together a covalent bond. This peptide is an example of a highly generic
CC sequence of the formula X-A-G-D-Y. A= K, Q or R; X= G-NH-CHM-CO, G-NH-CHM-
CC CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ,
CC NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or an amino protecting group; Z=
CC OH, NH2 or carboxy protecting group; or G and Z together are a covalent
CC bond or the gp. CO(CH2)aNH; a=1-12; R,U,V and W= peptide chains of 1-4
CC naturally occurring alpha aminoacids; M and Q= H, isopropyl, CHMe.Et,
CC phenyl, CH(OH).Me, 3-indolyl- or 4-imidazoly-methyl or (CH2)bT; b=1-6; T=
CC OH, MeO, MeS, Me2CH, phenyl (opt. 4-OH, substd), HS, NH2, COOH, CONH2, NH
CC C (NH) NH2; or M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f
CC or (CH2)eNH CO(CH2)gNH CO(CH2)f; c and d=1-4; e and f=1-6; g=1-12. The
CC peptide is a low mol. wt. deriv. of TNF. See also DE3841753-55,
CC DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 8 RKS 10

RESULT 16
AAR07719
ID AAR07719 standard; protein; 11 AA.
XX
AC AAR07719;
XX
DT 25-MAR-2003 (revised)

DT 22-FEB-1991 (first entry)
XX
DE Peptide fragment #5 from protease inhibitor Gelin.
XX
KW Gelin; protease inhibitor; Buffalo leeches; periodontal disease;
KW pulmonary emphysema; antibiotic.
XX
OS Hirudinaria manillensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= Asn, Ser
XX
PN WO9012808-A.
XX
PD 01-NOV-1990.
XX
PF 14-APR-1989; 89NL-00000943.
XX
PR 14-APR-1989; 89NL-00000943.
XX
PA (EUBI-) EURO-BIOPHARM TECHN.
XX
PI Atkinson A, Electricwa A, Sawyer RT, Vonsicard N, Voerman G;
XX
DR WPI; 1990-348426/46.
XX
PT Protease-inhibitor, gelin - is used in pharmaceutical, cosmetic and
PT dental compsns.
XX
PS Claim 3; Page 39; 57pp; English.
XX
CC The sequence is one of 6 fragments from Gelin, a protein with strong anti
CC -elastase and anti-chymotrypsin activity. Gelin is used to treat
CC periodontal diseases in mammals and can be used as an antibiotic against
CC bacteria. It may also inhibit germination of grains and seeds. The
CC polypeptide is isolated from leeches of the subfamily Hirudinariinae
CC ("Buffalo leeches"). The identity of residue 6 is unknown. See also
CC AAR07714-8 and AAR07720. (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 9 DMT 11

RESULT 17
AAR31358
ID AAR31358 standard; peptide; 11 AA.
XX
AC AAR31358;

XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1998 (first entry)
XX
DE Antimicrobial peptide #12 derived from bovine lactoferrin.
XX
KW antimicrobial agent; iron-binding protein; athlete's foot; mastitis;
KW antibacterial agent.
XX
OS Synthetic.
XX
PN EP503939-A1.
XX
PD 16-SEP-1992.
XX
PF 12-MAR-1992; 92EP-00302125.
XX
PR 13-MAR-1991; 91JP-00048196.
PR 24-APR-1991; 91JP-00094492.
PR 24-APR-1991; 91JP-00094493.
XX
PA (MORG) MORINAGA MILK IND CO LTD.
XX
PI Tomita M, Kawase K, Takase M, Bellamy WR, Yamauchi K;
PI Wakabayashi H, Tokita Y;
XX
DR WPI; 1992-310006/38.
XX
PT New antimicrobial peptide(s) - active against e.g. Listeria
PT monocytogenes, Staphylococcus aureus, Pseudomonas aeruginosa and
PT Klebsiella pneumoniae, for treating e.g. diarrhoea, mastitis, etc.
XX
PS Claim 8; Page 17; 19pp; English.
XX
CC This synthetic peptide has a sequence derived from bovine lactoferrin.
CC The peptide has stronger antimicrobial activity than unhydrolysed
CC lactoferrin and improved heat resistance. The peptide had a minimum
CC inhibitory concentration (microM) of 1.5, 3, 6 and 25 against Listeria
CC monocytogenes, Staphylococcus aureus, Pseudomonas aeruginosa and
CC Klebsiella pneumoniae, respectively. This and other peptides derived from
CC hydrolysed lactoferrin can be incorporated into foods, human or
CC veterinary compositions (e.g. for treating mastitis and athlete's foot),
CC toiletries, cosmetics, cleaning agents, etc. See AAR31350-R31361.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 1 KSR 3

AAR32352

ID AAR32352 standard; peptide; 11 AA.

XX

AC AAR32352;

XX

DT 05-JUL-1993 (first entry)

XX

DE Human Factor X peptide.

XX

KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin;

KW formation; Factor Xa; pathway mediated activation; inhibition.

XX

OS Synthetic.

XX

PN US5187155-A.

XX

PD 16-FEB-1993.

XX

PF 23-JUN-1989; 89US-00371561.

XX

PR 23-JUN-1989; 89US-00371561.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Fair DS;

XX

DR WPI; 1993-075751/09.

XX

PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit

PT factor X activation and/or Factor Xa function, useful for preventing

PT blood clot formation and treating deep vein thrombosis, pulmonary

PT embolism, etc.

XX

PS Example; Page 6; 23pp; English.

XX

CC The sequence is that of a peptide corresponding to amino acids 404-414 of
CC the human factor X molecule which was tested for its effect, (as a % of
CC the control rate), on the rate of Factor Xa formation and on the rate of
CC thrombin formation. The results obtd. were for activation of Factor X by
CC the extrinsic activation complex 78%, by the intrinsic activation complex
CC 98%, and activation by RVV-X, 76%. For the rate of thrombin formation the
CC rate was 88% as compared to the control rate

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3

|||

Db 1 ARK 3

RESULT 19

AAR43465

ID AAR43465 standard; peptide; 11 AA.

XX
AC AAR43465;
XX
DT 25-MAR-2003 (revised)
DT 12-MAY-1994 (first entry)
XX
DE Ro/SSA epitope 280.
XX
KW Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;
KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;
KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';
KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO9321223-A1.
XX
PD 28-OCT-1993.
XX
PF 13-APR-1993; 93WO-US003484.
XX
PR 13-APR-1992; 92US-00867819.
XX
PA (OKLA) UNIV OKLAHOMA STATE.
XX
PI Harley JB;
XX
DR WPI; 1993-351658/44.
XX
PT New linear epitope(s) for human auto-antibodies - from the Ro/SSA, La/SSB
PT and Sm B/B' antigens and ribo:nucleoprotein, used for diagnosing and
PT treating auto-immune disorders e.g. systemic lupus erythematosus.
XX
PS Claim 1; Page 31; 43pp; English.
XX
CC The sequences given in AAR43391-562 are linear epitopes which are derived
CC from the 60 kD Ro/SSA peptide, the La/SSB autoantigen, the 70 kD nuclear
CC ribonucleoprotein (nRNP) and the Sm B/B' polypeptide. These antigens are
CC common in systemic lupus erythematosus (SLE) and closely related
CC disorders. The Ro/SSA family of proteins has been shown to have several
CC molecular forms which are defined by the molecular weight of the antigen
CC identified. The major form has a molecular weight of 60 kD and two
CC additional forms have molecular weights of 52 and 54 kD. La/SSB is also a
CC member of this group of autoantibodies and binds small RNAs with a
CC polyuridine terminus. La/SSB is bound by a third of the anti-Ro/SSA
CC precipitin positive sera. La/SSB has been shown to be a 46-50 kD
CC monomeric phosphoprotein which associates with RNA polymerase III
CC transcripts. Anti-Sm antibodies precipitate snRNPs containing the U1, U2,
CC U4/U6 and U5 RNA. Anti-Sm antibodies may be directed against one or a
CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD), E/F
CC (11 kD doublet) and G (less than 10 kD). These epitopes may be used for
CC preventing, treating or screening autoimmune disorders, especially SLE or
CC Sjogrens syndrome (SS). They bind to a human autoantibody and may
CC therefore be used as vaccines. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9
|||
Db 9 MTA 11

RESULT 20

AAR45170

ID AAR45170 standard; protein; 11 AA.

XX

AC AAR45170;

XX

DT 25-MAR-2003 (revised)

DT 16-JUN-1994 (first entry)

XX

DE Listeria p60 peptide epitope.

XX

KW Listeria monocytogenes; antibodies; immunoassay; conjugate.

XX

OS Synthetic.

XX

PN DE4318450-A1.

XX

PD 16-DEC-1993.

XX

PF 03-JUN-1993; 93DE-04318450.

XX

PR 11-JUN-1992; 92DE-04219111.

PR 25-NOV-1992; 92DE-04239567.

XX

PA (MERE) MERCK PATENT GMBH.

XX

PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;

PI Hofmann G, Bubert A, Goebel W, Koehler S;

XX

DR WPI; 1993-406956/51.

XX

PT New primers for PCR detection of Listeria - including individual species,
PT also new peptide(s) for raising antibodies for immunochemical detection.

XX

PS Disclosure; Fig 2; 19pp; German.

XX

CC The sequence is that of a Listeria p60 peptide epitope which may be
CC used in the prodn. of antibodies for the detection of Listeria by
CC immunoassay (partic. ELISA). It may be used as part of a method that
CC allows determination of individual Listeria species, esp. L.
CC monocytogenes. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AIK 11
|||
Db 2 AIK 4

RESULT 21

AAR70606

ID AAR70606 standard; peptide; 11 AA.

XX

AC AAR70606;

XX

DT 14-FEB-1996 (first entry)

XX

DE HIV(B35)ARV2-7, human immunodeficiency virus epitope.

XX

KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;

KW binding peptide; induce killer cell; prevention; treatment; AIDS;

KW autoimmune disease syndrome; vaccine.

XX

OS Human immunodeficiency virus.

XX

PN WO9511255-A1.

XX

PD 27-APR-1995.

XX

PF 19-OCT-1994; 94WO-JP001756.

XX

PR 19-OCT-1993; 93JP-00261302.

XX

PA (AJIN) AJINOMOTO KK.

XX

PI Takiguchi M, Miwa K;

XX

DR WPI; 1995-170188/22.

XX

PT HLA-binding peptide fragments from HIV proteins - induce killer cells

PT which target HIV-infected cells and can be incorporated into anti-HIV

PT vaccines.

XX

PS Example 1; Page 10; 61pp; Japanese.

XX

CC AAR70606 is a peptide fragment derived from an HIV (Human
CC Immunodeficiency Virus) protein and is capable of binding to a human
CC lymphocyte antigen. The peptide can induce killer cells which target HIV-
CC infected cells. It is also useful in the prevention and treatment of HIV
CC and AIDS. Anti-HIV vaccines may incorporate the peptides, or may
CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the
CC peptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 RKS 4

Db

|||
7 RKS 9

RESULT 22

AAR79902

ID AAR79902 standard; peptide; 11 AA.

XX

AC AAR79902;

XX

DT 19-MAR-1996 (first entry)

XX

DE Human FK-506 cytosolic binding protein FKBP12 residues 38-48.

XX

KW Human; cytosolic binding protein; FKBP12; residues 38-48; FK-506; diagnosis; purification; determination; detection; immunosuppressant; binding partner; antibodies.

XX

OS Homo sapiens.

XX

PN WO9521861-A1.

XX

PD 17-AUG-1995.

XX

PF 10-FEB-1995; 95WO-US001721.

XX

PR 15-FEB-1994; 94US-00197795.

XX

PA (MERI) MERCK & CO INC.

XX

PI Wiederrecht GJ, Sewell TJ;

XX

DR WPI; 1995-293076/38.

XX

PT New FK-506 cytosolic binding protein - used for diagnostic, purification or investigational procedures, partic. for detection of FK-506.

XX

PS Disclosure; Page 9; 68pp; English.

XX

CC AAR79900-R79902 are peptides from the human FK-506 immunosuppressant
CC cytosolic binding protein FKBP12. The peptides were conjugated to
CC thyroglobulin, and used to generate anti-peptide antibodies. The
CC antibodies were used to survey tissue and cell extracts relevant to the
CC immunosuppressive effects FK-506. FKBP12 can be used as a specific
CC binding partner for a variety of ligands for diagnostic, purifcn. and
CC investigatory procedures. It can also be used to determine the presence
CC or quantity of FK-506 in a sample, e.g. a body fluid from an
CC immunosuppressed individual on FK-506 therapy

XX

SQ Sequence 11 AA;

Query Match 27.38; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

4 SRD 6

|||

RESULT 23

AAR64598

ID AAR64598 standard; peptide; 11 AA.

XX

AC AAR64598;

XX

DT 25-MAR-2003 (revised)

DT 01-SEP-1995 (first entry)

XX

DE RF-1 peptide 43 from respiratory syncitial virus.

XX

KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix; leucine zipper; DP-185; respiratory syncitial virus; RSV.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	1 /note= "optionally has an amino, acetyl, 9-fluorenylmethoxy-carbonyl, hydrophobic or macromolecular carrier gp. attached"
FT	Modified-site	11 /note= "optionally has a carboxyl, amido, hydrophobic or macromolecular carrier gp. attached"

XX

PN WO9428920-A1.

XX

PD 22-DEC-1994.

XX

PF 07-JUN-1994; 94WO-US005739.

XX

PR 07-JUN-1993; 93US-00073028.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;

PI Petteway SR;

XX

DR WPI; 1995-036105/05.

XX

PT Computer search generated synthetic peptides - are inhibitors of HIV transmission.

XX

PS Claim 14; Page 138; 182pp; English.

XX

CC AAR64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived from respiratory syncitial virus (RSV) (AAR64590) which have been truncated at the amino terminus. The peptides are DP-178 like peptides. CC DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI CC transmembrane protein gp41. It forms a putative alpha helix at the C- CC terminal end of the gp41 ectodomain, and complexes with DP-107 CC (corresponds to amino acids 558-595) which contains a leucine zipper CC motif. The peptides complex via non-covalent protein-protein

CC interactions. The peptide derivatives were identified by a computer
CC assisted peptide sequence search. The antiviral activity of this peptide
CC is not stated in the specification. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
 |||
Db 5 RKS 7

RESULT 24

AAR96813

ID AAR96813 standard; peptide; 11 AA.

XX

AC AAR96813;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human laminin b2 fragment, homologous to N.gonorrhoeae MS11 IgAP.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;
KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;
KW human laminin b2; Neisseria gonorrhoeae.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
FT Region 1. .5
FT /note= "identical to sequence in Neisseria gonorrhoeae
IgAP"
FT Region 7
FT /note= "identical to corresponding residue in Neisseria
gonorrhoeae IgAP"
FT Region 10. .11
FT /note= "identical to sequence in Neisseria gonorrhoeae
IgAP"

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;
PI Oetzelberger KB;

XX

DR WPI; 1996-188456/19.

XX
PT Medicaments for treating auto-immune or viral diseases - contg.
PT substances interfering with bacterial poly:protein function.
XX
PS Claim 32; Fig 2; 117pp; German.
XX
CC The present sequence from human laminin b2 has homology to a cleavage
CC product from the IgA domain of the precursor of IgA-protease polyprotein
CC (IPP) of *Neisseria gonorrhoeae* strain MS11. The *Neisseria* IPP has been
CC implicated in rheumatoid arthritis and other auto-immune diseases. The
CC polyprotein also activates proviruses, including HIV. Substances which
CC interfere with the function of IPP from *Neisseria* will be useful for
CC treating associated autoimmune diseases and viral infections. Peptides
CC comprising the homology region sequences, whether from *Neisseria* or from
CC humans, are claimed
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 3 ARK 5

RESULT 25
AAR96812
ID AAR96812 standard; peptide; 11 AA.
XX
AC AAR96812;
XX
DT 16-OCT-2003 (revised)
DT 29-NOV-1996 (first entry)
XX
DE *N.gonorrhoeae* MS11 IgA domain, homologous to human laminin b2.
XX
KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;
KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;
KW human laminin b2.
XX
OS *Neisseria gonorrhoeae*; MS11.
XX
FH Key Location/Qualifiers
FT Region 1..5
FT /note= "identical to sequence in human laminin b2"
FT Region 7
FT /note= "identical to corresponding residue in human
FT laminin b2"
FT Region 10..11
FT /note= "identical to sequence in human laminin b2"
XX
PN WO9609395-A2.
XX
PD 28-MAR-1996.
XX

PF 21-SEP-1995; 95WO-EP003726.
XX
PR 21-SEP-1994; 94DE-04433708.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;
PI Oetzelberger KB;
XX
DR WPI; 1996-188456/19.
XX
PT Medicaments for treating auto-immune or viral diseases - contg.
PT substances interfering with bacterial poly:protein function.
XX
PS Claim 32; Fig 2; 117pp; German.
XX
CC The present sequence is a cleavage product from the IgA domain of the
CC precursor of IgA-protease polyprotein (IPP) of *Neisseria gonorrhoeae*
CC strain MS11. The *Neisseria* IPP has marked homology to certain human
CC proteins and has been implicated in rheumatoid arthritis and other auto-
CC immune diseases. The polyprotein also activates proviruses, including
CC HIV. Substances which interfere with the function of IPP from *Neisseria*
CC will be useful for treating associated autoimmune diseases and viral
CC infections. The present peptide is homologous to human laminin b2.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 3 ARK 5

RESULT 26
AAR96834
ID AAR96834 standard; peptide; 11 AA.
XX
AC AAR96834;
XX
DT 16-OCT-2003 (revised)
DT 29-NOV-1996 (first entry)
XX
DE *N.gonorrhoeae* IgA alpha1 region, homologous to human Nfh protein.
XX
KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;
KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;
KW human neurofilament triplet h protein; Nfh.
XX
OS *Neisseria gonorrhoeae*; MS11.
XX
FH Key Location/Qualifiers
FT Region 1..3
FT /note= "identical to sequence in human neurofilament

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
Db 7 ARK 9

RESULT 27
AAW15309
ID AAW15309 standard; peptide; 11 AA.
XX
AC AAW15309;
XX
DT 01-JUL-1997 (first entry)

XX
DE 78 kDa glucose regulated protein.
XX
KW Release; expression; secretion; mammal; foetus; trophoblast; cell;
KW chorionic villus; unchanged; hypoxia; marker; indicator; abnormal;
KW maternal; placental; interface; function; abortion; screening;
KW intrauterine; growth; retardation; gestation; disease; tumour; molar;
KW pregnancy; choriocarcinoma; ectopic; apolipoprotein a-1; proteinuria;
KW hypertension; preeclampsia; induction; mitigation;
KW glucose regulated protein; 78 kDa; control.
XX
OS Homo sapiens.
XX
PN WO9633214-A2.
XX
PD 24-OCT-1996.
XX
PF 18-APR-1996; 96WO-US005441.
XX
PR 18-APR-1995; 95US-00423409.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Fisher SJ, Genbacev O, Foulk R, Clauser KR, Burlingame AL;
XX
DR WPI; 1996-497265/49.
XX
PT Detection of abnormal placental function or metastases - by detecting
PT proteins with altered expression or trophoblasts or chorionic villi under
PT hypoxic conditions.
XX
PS Example 2; Page 40; 57pp; English.
XX
CC The level of release of the present peptide by a mammalian foetal
CC trophoblast cell or a chorionic villus is unchanged when the cell or
CC villus is grown under hypoxic conditions, characterised by a partial
CC pressure of oxygen (pO₂) of 14 mm Hg. The peptide can be used as a
CC control marker for the presence of hypoxic conditions indicative of an
CC abnormal maternal-placental interface, and consequent abnormal placental
CC function in, e.g. threatened abortion, intrauterine growth retardation,
CC gestational trophoblast diseases including molar pregnancy,
CC choriocarcinoma, placental site tumours, ectopic pregnancy, proteinuria,
CC pregnancy induced hypertension and preeclampsia. It can also be used as a
CC control in screens for inducers or mitigators of abnormal maternal-
CC placental interface
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10
|||
Db 4 TAI 6

RESULT 28
AAW32498
ID AAW32498 standard; peptide; 11 AA.
XX
AC AAW32498;
XX
DT 21-APR-1998 (first entry)
XX
DE Helicostatin 9, which inhibits gut motility in the blowfly.
XX
KW Blowfly; callatostatin; insect neuropeptide; Leu-callatostatin;
KW gut motility; cockroach; insecticide; blowfly; cydiastatin; helicostatin.
XX
OS Helicoverpa armigera.
XX
PN WO9735981-A1.
XX
PD 02-OCT-1997.
XX
PF 26-MAR-1997; 97WO-GB000843.
XX
PR 26-MAR-1996; 96GB-00006272.
XX
PA (QUEE-) QUEEN MARY & WESTFIELD COLLEGE.
XX
PI Thorpe A, Duve H, Johnsen AH, East P;
XX
DR WPI; 1997-489644/45.
XX
PT New callatostatin-like peptide(s) and DNA - are active as inhibitors of
PT gut motility, used as insecticides, particularly against lepidopteran
PT insects.
XX
PS Claim 4; Page 63; 92pp; English.
XX
CC The present sequence represents a specifically claimed callatostatin-
CC like peptide which is active as an inhibitor of gut motility. The
CC callostatin-like peptides can be used as insecticides, particularly
CC against lepidopteran insects. The invention relates to novel recombinant
CC or isolated DNA sequences representing the Helicoverpa armigera
CC helicostatin gene, the DraI fragment from Calliphora vomitoria or the
CC Lucilia cuprina prohormone coding sequence. These sequences encode
CC proteins of 228, 177 and 179 amino acids respectively
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RDM 7
|||
Db 2 RDM 4

RESULT 29
AAW41012

ID AAW41012 standard; peptide; 11 AA.
XX
AC AAW41012;
XX
DT 22-APR-1998 (first entry)
XX
DE Anti-glutathione antibody fragment VH1; DP-25.
XX
KW Antibody; glutathione; human; detection.
XX
OS Homo sapiens.
XX
PN JP09154583-A.
XX
PD 17-JUN-1997.
XX
PF 05-DEC-1995; 95JP-00316872.
XX
PR 05-DEC-1995; 95JP-00316872.
XX
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
XX
DR WPI; 1997-367063/34.
XX
PT Recombinant anti:glutathione antibody - useful for detection and
PT determination of glutathione.
XX
PS Claim 2; Page 10; 15pp; Japanese.
XX
CC This sequence represents a fragment of the antibody of the invention. The
CC antibody of the invention is an antibody which combines with glutathione
CC and with a protein modified by glutathione. The anti-glutathione antibody
CC is useful for detection and determination of glutathione
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 7 KSR 9

RESULT 30
AAW40399
ID AAW40399 standard; protein; 11 AA.
XX
AC AAW40399;
XX
DT 17-OCT-2003 (revised)
DT 23-JUL-1998 (first entry)
XX
DE NNOS binding peptide #1.
XX
KW Nitric oxide synthase; endothelial; ENOS; INOS; inducible; NNOS;

KW neuronal; calmodulin; brain damage; shock; autoimmune disease; inflammatory condition; multiple sclerosis; diabetes; dementia; dysplasia; cancer; infectious disease; cytotoxic; hypertension; atherosclerosis; asthma; detection; screening.
XX
OS unidentified.
XX
PN WO9802555-A1.
XX
PD 22-JAN-1998.
XX
PF 10-JUL-1997; 97WO-US012568.
XX
PR 12-JUL-1996; 96US-00679006.
XX
PA (SALE/) SALERNO J. C.
XX
PI Salerno JC;
XX
DR WPI; 1998-110601/10.
XX
PT New modulators of nitric oxide synthase - used for treating e.g. toxic shock, auto-immune disease, inflammatory disease, diabetes, hypertension, infections or cancer.
XX
PS Claim 14; Page 41; 78pp; English.
XX
CC This sequence represents a peptide which binds adjacent to the calmodulin binding site of neuronal nitric oxide synthase (NNOS). This peptide is used in a novel method which identifies an agent which inhibits nitric oxide synthase (NOS) by blocking calmodulin (CAM) activation of the NOS. Such agents which modulate NOS activity can be used to treat a disease or condition associated with nitric oxide production. Agents which inhibit neuronal NOS (NNOS) can be used to prevent brain damage in conditions involving cerebral ischaemia or reperfusion injury, such as head trauma. Agents which decrease the activity of inducible NOS (iNOS) can be used to treat a condition modulated by production of NO by iNOS, such as septic shock, toxic shock, autoimmune disease such as rheumatoid arthritis, inflammatory conditions such as inflammatory bowel disease, multiple sclerosis, diabetes, or to combat dementia, immune system destruction, and/or physical deterioration in individuals infected with the AIDS virus. Agents which activate iNOS can be used to treat disease relating to dysplasia, cancer, or infectious disease. Activation of iNOS can produce cytotoxic levels of NO which would aid in the elimination of dysplastic or cancerous tissue, or aid in the control of infectious agents such as viruses, microbes, or other parasites. Agents which increase the activity of endothelial NOS (eNOS) can be used to treat a condition modulated by production of NO by eNOS such as hypertension, atherosclerosis or acute asthma. An agent which activates eNOS or NNOS in the corpus cavernosa can be used for treating male erectile dysfunction. The products and methods can also be used for detection and drug screening. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 4 RKS 6

RESULT 31

AAW62282

ID AAW62282 standard; peptide; 11 AA.

XX

AC AAW62282;

XX

DT 24-SEP-1998 (first entry)

XX

DE Synthetic immunoglobulin TVG 405 light chain CDR3 peptide.

XX

KW HPV16; human papilloma virus; epithelial tumour; cervical cancer;
KW precancerous cervical lesion; screening; detection; infection; cervix;
KW HPV E4; immunoglobulin; antibody.

XX

OS Synthetic.

OS Human papillomavirus.

XX

PN WO9825145-A1.

XX

PD 11-JUN-1998.

XX

PF 03-DEC-1997; 97WO-GB003321.

XX

PR 03-DEC-1996; 96GB-00025142.

PR 05-SEP-1997; 97GB-00018745.

XX

PA (MEDI-) MEDICAL RES COUNCIL.

XX

PI Doorbar J;

XX

DR WPI; 1998-333497/29.

XX

PT Detecting papilloma virus infection using molecule binding to E4 protein
PT - useful, e.g. in screening for pre-cancerous cervical lesions and to
PT determine type(s) of human papilloma virus infecting human patients.

XX

PS Example 2; Page 17; 52pp; English.

XX

CC A new method has been developed for detecting a papilloma virus infection
CC in an organism. The method comprises: (i) obtaining a sample of cells
CC from the potential infection site; (ii) contacting the cells with a
CC molecule binding specifically to papilloma virus E4 protein, and (iii)
CC monitoring the binding. The method is useful to detect papilloma virus
CC infections in organisms (especially mammals) and especially HPV
CC infections (e.g. with HPV16, 18, 33, 35, 45, 51, 56, 58 or 61) in humans.
CC Papilloma viruses cause epithelial tumours in humans varying in severity
CC depending on the infection site and HPV type involved. The method is
CC particularly useful to determine papilloma infection in the mammalian
CC cervix and especially to screen for pre-cancerous cervical lesions in
CC humans, since over 90% of cervical carcinoma patients show cervical HPV

CC infection. It is also useful to determine the type(s) of HPV infection in
CC a patient, by using a molecule binding specifically to a subset of HPV E4
CC proteins. This is important, since progression to malignant disease (and
CC hence clinical prognosis) is dependent on HPV type. Molecules capable of
CC binding E4 are also useful to target anticancer/antiviral agents capable
CC of destroying papilloma viruses and/or papilloma virus-infected cells.
CC The present sequence represents a synthetic immunoglobulin TVG 405 light
CC chain CDR3 peptide, from an example of the present invention
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 32

AAW41078

ID AAW41078 standard; peptide; 11 AA.

XX AC AAW41078;

XX DT 05-MAY-1998 (first entry)

XX DE ADPHK protein sequence fragment, SEQ ID NO 3.

XX KW ADPHK; enzyme; hexokinase; hexose 6-phosphate; adenosine 1-phosphate;

KW adenosine 2-phosphate; hexose.

XX OS Synthetic.

XX PN JP09327297-A.

XX PD 22-DEC-1997.

XX PF 12-MAR-1997; 97JP-00057330.

XX PR 15-MAR-1996; 96JP-00059136.

XX PA (ASAHI) ASAHI KASEI KOGYO KK.

XX DR WPI; 1998-104115/10.

DR N-PSDB; AAV03982.

XX PT DNA sequence encoding hexokinase - is used to transform organism for

PT production of enzyme.

XX PS Disclosure; Page 16; 17pp; Japanese.

XX CC This sequence represents a fragment of the enzyme of the invention. The

CC enzyme of the invention is designated ADPHK, and is a hexokinase. The DNA

CC encoding this sequence was used to isolate the enzyme from *P. furiosus* or

CC *T. litoralis*. The hexokinase of the invention is capable of catalysing

CC the formation of hexose 6-phosphate and adenosine 1-phosphate from
CC adenosine 2-phosphate and hexose. The new DNA sequence is used to
CC transform the microorganism which is capable of producing a hexokinase.
CC The recombinant microorganism is highly efficient at producing the enzyme
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 8 AIK 10

RESULT 33
AAW46000
ID AAW46000 standard; peptide; 11 AA.
XX
AC AAW46000;
XX
DT 03-JUL-1998 (first entry)
XX
DE Peptide #25 based on mouse SSTR 2 (residues 31-41).
XX
KW Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;
KW insulin-like growth factor binding protein; ILGFBP; SSTR; diabetes;
KW somatostatin receptor; insulin-like growth factor.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9744352-A1.
XX
PD 27-NOV-1997.
XX
PF 22-MAY-1997; 97WO-AU000312.
XX
PR 22-MAY-1996; 96AU-00009990.
XX
PA (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
XX
PI Gerraty NL, Westbrook SL, Kingston DJ;
XX
DR WPI; 1998-018427/02.
XX
PT New non-naturally occurring peptide(s) - which are based on portions of
PT somatostatin, somatostatin receptors and insulin-like growth factor
PT binding protein.
XX
PS Disclosure; Page 9; 136pp; English.
XX
CC Peptides AAW45983-W456025 are based on portions of somatostatin,
CC somatostatin receptors (SSTR) and insulin-like growth factor binding
CC proteins (IGFBP). They are capable of increasing weight gain, birth
CC weight, growth rates, milk production, levels of circulating insulin, IGF

CC -I and IGF-III, fibre production and muscle weight. They may be used to
CC modulate carbohydrate metabolism and in treatment of diabetes. The oil
CC carrier may be used for delivery of the peptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 34

AAY20426

ID AAY20426 standard; protein; 11 AA.

XX

AC AAY20426;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human microtubule associated protein 2 mutant fragment 122.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB000705.

XX

PR 10-APR-1997; 97US-0043163P.

XX

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.

XX

PI Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX

DR WPI; 1998-609901/51.

DR N-PSDB; AAX75757.

XX

PT Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
PS Disclosure; Fig 6; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 7 RKS 9

RESULT 35
AAW61162
ID AAW61162 standard; peptide; 11 AA.
XX
AC AAW61162;
XX
DT 26-OCT-1998 (first entry)
XX
DE IgE derived oligopeptide 1.
XX
KW IgE Fc epsilon receptor; Cysteine; disulphide bond; loop structure;
KW anti-allergy treatment; anaphylactic immune response; antibody;
KW Type I hypersensitivity; hay fever; asthma.
XX
OS Homo sapiens.
XX
PN WO9824808-A2.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-US022348.

XX
PR 06-DEC-1996; 96US-0031991P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Padlan EA, Birgit AH;
XX
DR WPI; 1998-333254/29.
XX
PT Oligopeptide interacting with human IgE Fc epsilon receptor - useful in
PT anti-allergy treatment as competitors of human IgE for Fc epsilon
PT receptor to block development of Type I hypersensitivity.
XX
PS Claim 1; Page 3; 45pp; English.
XX
CC The sequences AAW61162-W61166 are IgE derived oligopeptides which
CC interact with the human IgE Fc epsilon receptor. This particular
CC oligopeptide is the core minimal region of IgE required for interaction
CC with these Fc epsilon receptors and can thus bind both high and low
CC affinity receptors. The peptide was derived from a region of the epsilon
CC heavy chain of IgE, and can therefore mimic and block human IgE binding
CC to the Fc receptors. This sequence was used as the core sequence in the
CC other oligopeptides that were derived, they varied in length and at their
CC N and C terminal end. The IgE protein forms a loop structure naturally,
CC thus the addition of Cysteine residues at both ends of this sequence
CC enables disulphide bonds to form which results in a loop structure. These
CC oligopeptides are small and are thus easy to synthesise and deliver, they
CC are stable, highly active in anti-allergy treatment and lastly are less
CC likely to trigger an adverse anaphylatic immune response. The
CC oligopeptides can be used as competitors of human IgE for the Fc epsilon
CC receptor in anti-allergy treatment. Human IgE mediates Type I
CC hypersensitivity, an allergic response producing symptoms such as hay
CC fever and asthma. Thus the oligopeptides can be used to block the
CC development of type I hypersensitivity
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 9 RKS 11

RESULT 36
AAY03092
ID AAY03092 standard; peptide; 11 AA.
XX
AC AAY03092;
XX
DT 08-JUN-1999 (first entry)
XX
DE New nociceptin analogue #74 from WO9903880.
XX
KW Nociceptin; vasomotor disorder; menopausal hot flush; opioid antagonist;

KW hyperalgesia; neuroendocrine secretion; stress; locomotor activity; anxiety; instinctive behaviour; learning disorder; memory disorder; attention disorder; sensory perception disorder.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Modified-site 6. .10
FT /note= "the side chains of residues 6 and 10 are
FT condensed via a Gly residue to form a lactam bridge
FT between these two positions"
FT Modified-site 10
FT /label= Orn
FT /note= "ornithine residue"
FT Modified-site 11
FT /note= "C-terminal amide"

XX

PN WO9903880-A1.

XX

PD 28-JAN-1999.

XX

PF 13-JUL-1998; 98WO-DK000326.

XX

PR 15-JUL-1997; 97DK-00000867.

PR 17-JUL-1997; 97US-0052862P.

XX

PA (NOVO) NOVO-NORDISK AS.

XX

PI Thogersen H, Madsen K, Olsen UB, Johansen NL, Scheideler M;

XX

DR WPI; 1999-132156/11.

XX

PT New derivatives of nociceptin for treating vasomotor disorders -
PT specifically hot flushes in menopausal women.

XX

PS Claim 70; Page 61; 69pp; English.

XX

CC This sequence is a specifically claimed example of new nociceptin
CC analogue peptides which have the generic formula (X)_n-A1-A2-A3-A4-A5- A6-
CC A7-A8-A9-A10-A11-A12-A13-A14-A15-A16-A17-(Y)_m-A18, in which: A1 is
CC absent, a small or lipophilic amino acid, or phenylpropionic acid,
CC optionally acylated; A2 = aromatic, lipophilic or small amino acid,
CC optionally acylated if A1 is absent; A3, A6 and A7 = small, lipophilic or
CC polar amino acids; A2-A3 may alternatively be 5-amino-pentanoic, N-
CC methylanthranilic, 4-aminocyclohexane carboxylic or 3-aminomethyl-
CC benzoic acid; A4 = small, polar or aromatic amino acid; alternatively A3-
CC A4 = N-methylanthranilic acid; A5, A9, A10 and A11 = lipophilic or polar
CC amino acids; A8 = polar amino acids or D- or L-Ala; A12, A13, A14 and A15
CC = polar or lipophilic amino acids or may be absent; A16 and A17= small or
CC polar amino acids or may be absent; A18 = hydroxy or amino; X and Y =
CC polar, lipophilic, aromatic or small amino acids; n + m = 0-82; and two
CC or more of A1-A17, X and Y may be cyclisation amino acids, forming one or
CC more bridges (disulphide, lactam or Gly-lactam); provided that the
CC peptide has (a) at least two amino acids modifications relative to the
CC nociceptin sequence or (b) an unnatural amino acid at position A1. These
CC peptides are useful for treatment and prevention of vasomotor disorders,
CC specifically hot flushes in menopausal women. They can also be used for

CC antagonising the physiological effects of opioids and for treating
CC diseases related to hyperalgesia, neuroendocrine secretion, stress,
CC locomotor activity, anxiety, instinctive behaviour, and decrease in
CC learning, memory, curiosity, attention and/or sensory perception
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 7 ARK 9

RESULT 37

AAY29752

ID AAY29752 standard; protein; 11 AA.

XX

AC AAY29752;

XX

DT 08-NOV-1999 (first entry)

XX

DE Modified HBc amino acid sequence fragment K79.

XX

KW Human hepatitis B core protein; HBc; modified; immunodominant;

KW nucleocapsid protein; vaccine; T cell epitope.

XX

OS Hepatitis B virus.

OS Synthetic.

XX

PN WO9940934-A1.

XX

PD 19-AUG-1999.

XX

PF 11-FEB-1999; 99WO-US003055.

XX

PR 12-FEB-1998; 98US-0074537P.

XX

PA (IMMU-) IMMUNE COMPLEX CORP.

XX

PI Birkett AJ;

XX

DR WPI; 1999-527340/44.

DR N-PSDB; AAZ08826.

XX

PT Conjugate of hepatitis B core protein, modified to increase reactivity
PT with hapten, used to raise antibodies against the hapten, e.g. in
PT vaccines.

XX

PS Example 6; Page 112; 128pp; English.

XX

CC The present invention describes a conjugate (A) comprising a
CC strategically modified hepatitis B core (HBc) protein (I) attached to a
CC hapten, where (I) includes amino acids (aa) 10-140 of the wild type HBc
CC 183 aa sequence (given in AAY29674) and additionally has an insert (II)

CC in the region corresponding to aa's 50-100, where the insert is of 1 to
CC about 40 aa's and contains a chemically reactive aa residue linked to the
CC hapten. A vaccine containing (A), optionally in the form of particles, is
CC used to induce a protective antibody response against the pathogen from
CC which the hapten is derived, in humans or other animals. These pathogens
CC may be bacteria, viruses, rickettsia or protozoa. Insertion of (II)
CC overcomes the low reactivity of aa side chains in native HBc protein,
CC increasing the reactivity with hapten and resulting in conjugates of
CC improved immunogenicity. Modified HBc can be derivatised in the form of
CC particles by well-defined chemical methods, and is unlikely to cause
CC immunological side-effects. The present sequence represents a modified
CC HBc fragment, having a lysine insertion, from the present invention
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 8 SRD 10

RESULT 38

AAY47615

ID AAY47615 standard; peptide; 11 AA.

XX

AC AAY47615;

XX

DT 01-DEC-1999 (first entry)

XX

DE Immunogenic peptide having a human leukocyte antigen binding motif #2226.

XX

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9945954-A1.

XX

PD 16-SEP-1999.

XX

PF 13-MAR-1998; 98WO-US005039.

XX

PR 13-MAR-1998; 98WO-US005039.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX

DR WPI; 1999-551214/46.

XX

PT New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
XX
PS Claim 1; Page 116; 150pp; English.
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also known
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC (CTLs) which destroy antigen-bearing cells are normally induced by an
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC than the intact foreign antigen itself, and are particularly important in
CC tumour rejection and in fighting viral infections. The peptides are
CC therefore useful therapeutically to treat or prevent viral infections and
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC elicit an immune response in individuals susceptible or otherwise at risk
CC of viral infection or cancer, or used to treat chronic or acute
CC conditions. They are also useful diagnostically, and can be used to
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC patient. The polynucleotides encoding the immunogenic peptides are also
CC useful therapeutically and for immunisation as above
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10
|||
Db 6 TAI 8

RESULT 39
AAW74077
ID AAW74077 standard; peptide; 11 AA.
XX
AC AAW74077;
XX
DT 04-MAY-1999 (first entry)
XX
DE Fragment of gastro-intestinal transport receptor binding peptide.
XX
KW Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H;
KW hPEPT1; human; GI tract receptor; sucrose-isomaltase complex;
KW intestinal peptide-associated transporter; hypertension; diabetes;
KW osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
KW therapeutic agent delivery; therapy.
XX
OS Homo sapiens.
XX
PN WO9851325-A2.
XX

PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98WO-US010088.
XX
PR 15-MAY-1997; 97US-0046595P.
XX
PA (CYTO-) CYTOGEN CORP.
PA (ELAN-) ELAN CORP PLC.
XX
PI Alvarez VL, Omahony DJ, Lambkin IJ, Patterson CA, Singleton J;
PI Belinka BA, Carter JM, Cagney GM;
XX
DR WPI; 1999-009568/01.
XX
PT New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, or through, the gastrointestinal tract, e.g. insulin or leuprolide.
XX
PS Claim 18; Page 236; 294pp; English.
XX
CC This sequence represents a fragment of a protein of the invention. The invention relates to purified proteins (I) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal peptide-associated transporter (HPT1), hPEPT1, D2H and human sucrose-isomaltase complex (hSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, migraine, or angina pectoris. Specifically they are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (I) may also provide targeting to the GI tract. Other uses of (I) are: (i) to determine the level of specified receptors in a sample (in a binding assay); and (ii) to screen for molecules that bind (I). Immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and measure (I), e.g. for imaging, monitoring treatment, tissue analysis etc., also for peptide purification and immobilisation
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 3 RKS 5

RESULT 40
AAW74135
ID AAW74135 standard; peptide; 11 AA.
XX
AC AAW74135;
XX

DT 04-MAY-1999 (first entry)
XX
DE GI transport receptor binding protein fragment.
XX
KW Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H;
KW hPEPT1; human; GI tract receptor; sucrose-isomaltase complex;
KW intestinal peptide-associated transporter; hypertension; diabetes;
KW osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
KW therapeutic agent delivery; therapy; fusion protein.
XX
OS Homo sapiens.
XX
PN WO9851325-A2.
XX
PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98WO-US010088.
XX
PR 15-MAY-1997; 97US-0046595P.
XX
PA (CYTO-) CYTOGEN CORP.
PA (ELAN-) ELAN CORP PLC.
XX
PI Alvarez VL, Omahony DJ, Lambkin IJ, Patterson CA, Singleton J;
PI Belinka BA, Carter JM, Cagney GM;
XX
DR WPI; 1999-009568/01.
XX
PT New proteins that bind specifically to receptors in the gastro-intestinal
PT tract and related nucleic acid - chimaeras and antibodies, used to
PT deliver therapeutic or diagnostic agents to, or through, the
PT gastrointestinal tract, e.g. insulin or leuprolide.
XX
PS Disclosure; Page 195; 294pp; English.
XX
CC This sequence represents a fragment of a gastro-intestinal transport
CC protein binding peptide. The invention relates to purified proteins (I)
CC that bind specifically to at least one of the gastro-intestinal (GI)
CC tract receptors human intestinal peptide-associated transporter (HPT1),
CC hPEPT1, D2H and human sucrose-isomaltase complex (hSI). (I) provide
CC active transport of therapeutic agents through human and animal GI tissue
CC (into the blood) for in vivo delivery, particularly for treatment or
CC prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia,
CC cancer, migraine, or angina pectoris. Specifically they are used to
CC deliver insulin or leuprolide, but many other suitable therapeutic agents
CC are disclosed, including genes or inhibitory nucleic acid, imaging agents
CC and antigens. (I) may also provide targeting to the GI tract. Other uses
CC of (I) are: (i) to determine the level of specified receptors in a sample
CC (in a binding assay); and (ii) to screen for molecules that bind (I).
CC Immunogenic analogues or derivatives of (I) are used to raise antibodies
CC and in immunoassays. The antibodies are used to locate, detect and
CC measure (I), e.g. for imaging, monitoring treatment, tissue analysis
CC etc., also for peptide purification and immobilisation
XX
SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RKS 4
|||
Db 2 RKS 4

RESULT 41
AAW97473
ID AAW97473 standard; peptide; 11 AA.
XX
AC AAW97473;
XX
DT 19-MAY-1999 (first entry)
XX
DE Antigenic site of HN protein loop beta-2L01.
XX
KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.
XX
OS Sendai virus.
XX
PN WO9902695-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-NL000390.
XX
PR 08-JUL-1997; 97EP-00202100.
XX
PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.
XX
PI Langedijk JPM, Van Oirschot JT;
XX
DR WPI; 1999-120896/10.
XX
PT Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.
XX
PS Disclosure; Page 43; 63pp; English.
XX
CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification
CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4

Db

|||
9 RKS 11

RESULT 42

AAW97472

ID AAW97472 standard; peptide; 11 AA.

XX

AC AAW97472;

XX

DT 19-MAY-1999 (first entry)

XX

DE Antigenic site of HN protein loop beta-2L01.

XX

KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.

XX

OS Bovine parainfluenza virus.

XX

PN WO9902695-A2.

XX

PD 21-JAN-1999.

XX

PF 08-JUL-1998; 98WO-NL000390.

XX

PR 08-JUL-1997; 97EP-00202100.

XX

PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX

PI Langedijk JPM, Van Oirschot JT;

XX

DR WPI; 1999-120896/10.

XX

PT Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.

XX

PS Disclosure; Page 43; 63pp; English.

XX

CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification
CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 RKS 4

|||

Db

9 RKS 11

RESULT 43
AAW97476
ID AAW97476 standard; peptide; 11 AA.
XX
AC AAW97476;
XX
DT 19-MAY-1999 (first entry)
XX
DE Antigenic site of HN protein loop beta-2L01.
XX
KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.
XX
OS Mumps virus.
XX
PN WO9902695-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-NL000390.
XX
PR 08-JUL-1997; 97EP-00202100.
XX
PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.
XX
PI Langedijk JPM, Van Oirschot JT;
XX
DR WPI; 1999-120896/10.
XX
PT Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.
XX
PS Disclosure; Page 43; 63pp; English.
XX
CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification
CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 9 RKS 11

RESULT 44
AAW97477
ID AAW97477 standard; peptide; 11 AA.
XX

AC AAW97477;
XX
DT 19-MAY-1999 (first entry)
XX
DE Antigenic site of HN protein loop beta-2L01.
XX
KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.
XX
OS Newcastle disease virus.
XX
PN WO9902695-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-NL000390.
XX
PR 08-JUL-1997; 97EP-00202100.
XX
PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.
XX
PI Langedijk JPM, Van Oirschot JT;
XX
DR WPI; 1999-120896/10.
XX
PT Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.
XX
PS Disclosure; Page 43; 63pp; English.
XX
CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification
CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 9 RKS 11

RESULT 45
AAW97474
ID AAW97474 standard; peptide; 11 AA.
XX
AC AAW97474;
XX
DT 19-MAY-1999 (first entry)
XX

DE Antigenic site of HN protein loop beta-2L01.
XX
KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.
XX
OS Human parainfluenza virus.
XX
PN WO9902695-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-NL000390.
XX
PR 08-JUL-1997; 97EP-00202100.
XX
PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.
XX
PI Langedijk JPM, Van Oirschot JT;
XX
DR WPI; 1999-120896/10.
XX
PT Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.
XX
PS Disclosure; Page 43; 63pp; English.
XX
CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification
CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 9 RKS 11

RESULT 46
AAW97475
ID AAW97475 standard; peptide; 11 AA.
XX
AC AAW97475;
XX
DT 27-AUG-2003 (revised)
DT 19-MAY-1999 (first entry)
XX
DE Antigenic site of HN protein loop beta-2L01.
XX
KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;

KW virus epitope; attachment protein; vaccine; immunodominant epitope.
XX
OS Unidentified.
XX
PN WO9902695-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-NL000390.
XX
PR 08-JUL-1997; 97EP-00202100.
XX
PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.
XX
PI Langedijk JPM, Van Oirschot JT;
XX
DR WPI; 1999-120896/10.
XX
PT Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.
XX
PS Disclosure; Page 43; 63pp; English.
XX
CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification
CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RKS 4
|||
Db 9 RKS 11

RESULT 47
AAY02916
ID AAY02916 standard; protein; 11 AA.
XX
AC AAY02916;
XX
DT 11-JUN-1999 (first entry)
XX
DE Fragment of human secreted protein encoded by gene 98.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9902546-A1.
XX
PD 21-JAN-1999.
XX
PF 07-JUL-1998; 98WO-US013684.
XX
PR 08-JUL-1997; 97US-0051916P.
PR 08-JUL-1997; 97US-0051918P.
PR 08-JUL-1997; 97US-0051919P.
PR 08-JUL-1997; 97US-0051920P.
PR 08-JUL-1997; 97US-0051925P.
PR 08-JUL-1997; 97US-0051926P.
PR 08-JUL-1997; 97US-0051928P.
PR 08-JUL-1997; 97US-0051929P.
PR 08-JUL-1997; 97US-0051930P.
PR 08-JUL-1997; 97US-0051931P.
PR 08-JUL-1997; 97US-0051932P.
PR 08-JUL-1997; 97US-0052732P.
PR 08-JUL-1997; 97US-0052733P.
PR 08-JUL-1997; 97US-0052793P.
PR 08-JUL-1997; 97US-0052795P.
PR 08-JUL-1997; 97US-0052803P.
PR 18-AUG-1997; 97US-0055684P.
PR 18-AUG-1997; 97US-0055722P.
PR 18-AUG-1997; 97US-0055723P.
PR 18-AUG-1997; 97US-0055947P.
PR 18-AUG-1997; 97US-0055948P.
PR 18-AUG-1997; 97US-0055949P.
PR 18-AUG-1997; 97US-0055950P.
PR 18-AUG-1997; 97US-0055953P.
PR 18-AUG-1997; 97US-0055954P.
PR 18-AUG-1997; 97US-0055964P.
PR 18-AUG-1997; 97US-0055984P.
PR 18-AUG-1997; 97US-0056360P.
PR 12-SEP-1997; 97US-0058660P.
PR 12-SEP-1997; 97US-0058661P.
PR 12-SEP-1997; 97US-0058664P.
PR 12-SEP-1997; 97US-0058785P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fischer CL, Rosen CA, Soppet DR, Ruben SM, Kyaw H, Li Y, Zeng Z;
PI Lafleur DW, Moore PA, Shi Y, Olsen HS, Ebner R, Brewer LA;
XX
DR WPI; 1999-120770/10.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX

PS Disclosure; Page 115; 464pp; English.

XX

CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAX27302) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 123 novel genes and their fragments (nucleic acid sequences:
CC AAX27311-X27449; amino acid sequences AAY02650-Y02788) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 123 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAX27311 for
CC described uses)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 48

AAY89315

ID AAY89315 standard; peptide; 11 AA.

XX

AC AAY89315;

XX

DT 23-MAY-2000 (first entry)

XX

DE Core polypeptide fragment T No. 821.

XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW anti-fusogenic; differentiation factor; interleukin; interferon;
KW colony stimulating factor; hormone; angiogenic factor.

XX

OS Unidentified.

XX

PN WO9959615-A1.

XX

PD 25-NOV-1999.

XX

PF 20-MAY-1999; 99WO-US011219.

XX

PR 20-MAY-1998; 98US-00082279.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX

DR WPI; 2000-136792/12.

XX

PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

XX

PS Disclosure; Page 34; 124pp; English.

XX

CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 4 RKS 6

RESULT 49

AAY81922

ID AAY81922 standard; peptide; 11 AA.

XX

AC AAY81922;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.
XX
PS Example 2; Page 9; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 50
AAY81923
ID AAY81923 standard; peptide; 11 AA.
XX
AC AAY81923;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX

PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-00327536.
XX
PR 04-NOV-1998; 98JP-00327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.
XX
PS Example 2; Page 9; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 51
AAY81915
ID AAY81915 standard; peptide; 11 AA.
XX
AC AAY81915;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.

XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-00327536.
XX
PR 04-NOV-1998; 98JP-00327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl-acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal side.
XX
PS Claim 1; Page 8; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine protease. The invention relates to a quick assay method for asparagine protease of plant origin. The asparagine protease specifically recognises asparagine residues and cleaves proteins at the C-terminal end of the asparagine residue. The assay uses a fluorescence substrate (which has quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl group to the amino group of the glycine residue at the N-terminal side, and a 2,4-dinitrophenyl group to the C-terminal of an amino acid sequence. The fluorescence caused by the fluorescence substrate is not connected to the asparagine residue and can be measured after cleavage by the protease. The method is useful for assaying asparagine proteases of plant origin. The activity of the protease can be determined within a short time period and the enzyme activity can be measured with high sensitivity using the fluorescence substrate. The procedure is quick even when materials which inhibit other protease and fluorescence are included in the sample
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 52
AY81924
ID AY81924 standard; peptide; 11 AA.
XX
AC AY81924;
XX
DT 23-JUN-2000 (first entry)

XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-00327536.
XX
PR 04-NOV-1998; 98JP-00327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.
XX
PS Example 2; Page 9; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 53
AAY81916

ID AAY81916 standard; peptide; 11 AA.
XX
AC AAY81916;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-00327536.
XX
PR 04-NOV-1998; 98JP-00327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.
XX
PS Claim 1; Page 8; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||

RESULT 54
AAY81919
ID AAY81919 standard; peptide; 11 AA.
XX
AC AAY81919;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-00327536.
XX
PR 04-NOV-1998; 98JP-00327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.
XX
PS Claim 1; Page 9; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample
XX
SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 55
AAY81918
ID AAY81918 standard; peptide; 11 AA.
XX
AC AAY81918;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-00327536.
XX
PR 04-NOV-1998; 98JP-00327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.
XX
PS Claim 1; Page 9; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included

CC in the sample

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5

|||

Db 2 KSR 4

RESULT 56

AAY81920

ID AAY81920 standard; peptide; 11 AA.

XX

AC AAY81920;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;

KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl-acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal side.

XX

PS Claim 1; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine protease. The invention relates to a quick assay method for asparagine protease of plant origin. The asparagine protease specifically recognises asparagine residues and cleaves proteins at the C-terminal end of the asparagine residue. The assay uses a fluorescence substrate (which has quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl group to the amino group of the glycine residue at the N-terminal side, and a 2,4-dinitrophenyl group to the C-terminal of an amino acid sequence. The fluorescence caused by the fluorescence substrate is not connected to the asparagine residue and can be measured after cleavage by

CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5

|||

Db 2 KSR 4

RESULT 57

AAY81917

ID AAY81917 standard; peptide; 11 AA.

XX

AC AAY81917;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.

XX

PS Claim 1; Page 8; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has

CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 58

AAY81921

ID AAY81921 standard; peptide; 11 AA.

XX

AC AAY81921;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal
PT side.

XX

PS Example 2; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 59

AAB16453

ID AAB16453 standard; peptide; 11 AA.

XX

AC AAB16453;

XX

DT 27-OCT-2000 (first entry)

XX

DE Linear peptide that binds to angiostatin SEQ ID # 4.

XX

KW Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;
KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;
KW Helicobacter related disease; fracture; cat scratch fever.

XX

OS Synthetic.

XX

PN WO200032631-A2.

XX

PD 08-JUN-2000.

XX

PF 06-DEC-1999; 99WO-US028897.

XX

PR 04-DEC-1998; 98US-00206059.

XX

PA (ENTR-) ENTREMED INC.

XX

PI Macdonald NJ, Sim KL;
XX
DR WPI; 2000-412290/35.
XX
PT New angiogenesis-inhibiting protein receptors, useful in methods for
PT treating diseases and processes that are mediated by angiogenesis, such
PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
XX
PS Claim 1; Page 35; 100pp; English.
XX
CC This invention relates to angiogenesis-inhibiting protein receptors, and
CC the DNA sequences encoding them. Angiogenesis is the generation of new
CC blood vessels into a tissue, and normally occurs in wound healing, foetal
CC and embryonal development and the formation of the corpus luteum,
CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and
CC AAA68202) involved in angiogenesis, and has an amino acid sequence
CC similar to that of a plasminogen fragment (see murine plasminogen
CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.
CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and
CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein
CC sequences of human laminin. Laminin is an angiostatin binding protein,
CC and some of the peptides of the invention share homology with regions of
CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the
CC angiogenesis-inhibiting protein receptor fragments of the invention. The
CC peptides bind either angiostatin or endostatin and can be used in methods
CC for treating diseases and processes that are mediated by angiogenesis,
CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,
CC Crohn's disease, cerebral collaterals, arteriovenous malformations,
CC rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,
CC Helicobacter related diseases, fractures, placentation and cat scratch
CC fever. They are useful for the detection and prognosis of cancer. DNA
CC sequences A628204-A628241 encode the peptides of the invention
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 5 AIK 7

RESULT 60
AAY88542
ID AAY88542 standard; peptide; 11 AA.
XX
AC AAY88542;
XX
DT 07-AUG-2000 (first entry)
XX
DE NCAM Ig1 binding peptide #14.
XX
KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis; treatment; prosthetic nerve guide; treatment; nervous system.

XX
OS Synthetic.

XX
PN WO200018801-A2.

XX
PD 06-APR-2000.

XX
PF 23-SEP-1999; 99WO-DK000500.

XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.

XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.

XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX
DR WPI; 2000-293111/25.

XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX
PS Example 4; Page 25; 119pp; English.

XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas

CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart, CC liver and bowel may also be treated using the compound. The compound is CC used in a prosthetic nerve guide, and also to stimulate the ability to CC learn, and to stimulate the memory of a subject

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 1 ARK 3

RESULT 61

AAY88549

ID AAY88549 standard; peptide; 11 AA.

XX

AC AAY88549;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide #21.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1; KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis; KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia; KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis; KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 4; Page 25; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 62

AAB10140

ID AAB10140 standard; peptide; 11 AA.

XX

AC AAB10140;

XX

DT 10-NOV-2000 (first entry)

XX

DE Insertion sequence ISS1/1 Polymerase N-terminal protein fragment 39/2.

XX

KW Insertion sequence; ISS1/1; heat stable polymerase;
KW 3'-5'-exonuclease activity.

XX
OS Unidentified.
XX
PN DE19859107-A1.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1998; 98DE-01059107.
XX
PR 21-DEC-1998; 98DE-01059107.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Frey B, Sobek H, Schmitz-Agheguian G, Thomm M, Kath-Petersen R;
XX
DR WPI; 2000-476975/42.
XX
PT New heat-stable polymerase from ISS1/1, useful for amplification of,
PT labeling and extending nucleic acids, has 3'-5'- but not 5'-3'-
PT exonuclease activity.
XX
PS Example 8; Page 11; 40pp; German.
XX
CC This invention describes a novel heat-stable polymerase (I), from ISS1/1
CC which is homologous to PolI of Escherichia coli, that has 3'-5'-
CC exonuclease activity but lacks 5'-3'-exonuclease activity. (I), and their
CC mutated/modified forms with reduced 3'-exonuclease activity, are used for
CC labeling, amplifying and extending nucleic acids, especially in
CC polymerase chain reactions, but also e.g. for nick translation and for
CC random-priming labeling reactions. Mutation of (I) allow its 3'-5'-
CC exonuclease activity, very strong in the native enzyme, to be adjusted to
CC suit particular applications, while retaining its high processivity
CC (which can be increased further when used with associated proteins). (I)
CC can generate very long (over 2 kb) amplicons, which requires only small
CC amounts of template sequences, and reduces accumulation of errors. This
CC sequence represents an N-terminal fragment of the insertion sequence
CC ISS1/1 polymerase described in the method of the invention
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 9 AIK 11

RESULT 63
AAY93544
ID AAY93544 standard; peptide; 11 AA.
XX
AC AAY93544;
XX
DT 25-SEP-2000 (first entry)
XX

DE Amino acid sequence of a synthetic protein transduction domain.
XX
KW Protein transduction system; protein transduction domain;
KW cytotoxic domain; pathogen infection; retroviral infection;
KW plasmodial infection; cancer; prostate cancer.
XX
OS Synthetic.
XX
PN WO200034308-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029289.
XX
PR 10-DEC-1998; 98US-0111701P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF;
XX
DR WPI; 2000-431269/37.
XX
PT Protein transduction system for treating cancer and pathogenic infections
PT has a fusion protein comprising a protein transduction domain covalently
PT linked to a cytotoxic domain.
XX
PS Claim 66; Page 98; 127pp; English.
XX
CC AAY93542-51 represent synthetic protein transduction domains, which are
CC used in the protein transduction system of the invention. The
CC specification describes a protein transduction system, which comprises a
CC fusion protein. This fusion protein has a covalently linked protein
CC transduction domain and cytotoxic domain. The system is useful for
CC treating pathogen infection in mammals, infections such as those caused
CC by CMV, HSV-1, HCV, KSHV, yellow fever virus, flavivirus or rhinovirus,
CC retroviral infections such as HIV-1, HIV-2, HTLV-3 and/or LAV, plasmodial
CC infections associated with P.falciparum, P.vivax, P.ovale, P.malariae. It
CC is also useful for treating cancer, especially prostate cancer
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 64
AAB09423
ID AAB09423 standard; protein; 11 AA.
XX
AC AAB09423;
XX
DT 06-AUG-2003 (revised)

DT 30-AUG-2000 (first entry)
XX
DE Hepatitis GB virus protein sequence SEQ ID NO:550.
XX
KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
KW detection; characterisation; hepatitis.
XX
OS Hepatitis GB virus.
XX
PN US6051374-A.
XX
PD 18-APR-2000.
XX
PF 07-JUN-1995; 95US-00488445.
XX
PR 14-FEB-1994; 94US-00196030.
PR 13-MAY-1994; 94US-00242654.
PR 29-JUL-1994; 94US-00283314.
PR 23-NOV-1994; 94US-00344185.
PR 23-NOV-1994; 94US-00344190.
PR 30-JAN-1995; 95US-00377557.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX
DR WPI; 2000-338307/29.
XX
PT Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the HGBV
PT polynucleotide probe and detecting the complex that contains target HGBV.
XX
PS Example 18; Col 549-550; 369pp; English.
XX
CC The present invention describe a method for detecting target hepatitis GB
CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
CC containing HGBV. The method involves reacting (T) with a HGBV
CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
CC selectively hybridises to the HGBV genome or its full complement, and
CC detecting the complex that contains THN, indicating the presence of
CC target HGBV. The method is used for detecting target HGBV nucleic acid in
CC the test sample suspected of containing HGBV and for characterisation of
CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and
CC protein sequences used in the exemplification of the present invention.
CC (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||

RESULT 65

AY81393

ID AAY81393 standard; peptide; 11 AA.

XX

AC AAY81393;

XX

DT 19-JUN-2000 (first entry)

XX

DE PKC-alpha substrate peptide, used in detection of an SH-labelled oligo.

XX

KW Thermophilic rolling circle amplification; TRCA; circular template;

KW multimeric product; detection; single nucleotide polymorphism; SNP;

KW disulphide bond; PKC-alpha substrate; protein kinase C; fluorescent.

XX

OS Synthetic.

XX

PN WO200009738-A1.

XX

PD 24-FEB-2000.

XX

PF 17-AUG-1999; 99WO-US018808.

XX

PR 17-AUG-1998; 98US-0096830P.

PR 30-SEP-1998; 98US-00102535.

PR 03-NOV-1998; 98US-0106885P.

PR 03-NOV-1998; 98US-0106910P.

XX

PA (PACB) PACKARD BIOSCIENCE CO.

XX

PI Woodward KL, Nallur GN, Taylor S;

XX

DR WPI; 2000-224363/19.

XX

PT Analyzing a sample polynucleotide for detecting single nucleotide

PT polymorphism by rolling circle amplification.

XX

PS Example 29; Page 105; 126pp; English.

XX

CC The invention relates to methods for sensitively detecting the presence
CC of a particular nucleic acid in a sample, e.g., determining whether a
CC sequence of interest contains a particular genetic event such as a single
CC nucleotide polymorphism (SNP). The sample nucleotide to be analysed is
CC contacted with a single-stranded circular template comprising at least
CC one copy of a nucleotide sequence complementary to the sample sequence
CC and a type 2S restriction enzyme recognition site containing one or more
CC modified bases. The circular template is combined with nucleotide
CC triphosphates, a polymerase and optionally, a TRCA (thermophilic rolling
CC circle amplification) primer to yield a single stranded multimer
CC complementary in sequence to the circular template. A cleavage probe is
CC then added, which anneals to the type 2S restriction recognition sites in
CC the multimer and circular template, creating double stranded restriction
CC sites. On treatment with the appropriate enzyme, the multimer is cleaved
CC at the restriction sites, while the circular template is less sensitive
CC to cleavage, due to the presence of the modified base(s) in the

CC restriction site. The fragments produced can then be detected using an
CC array of capture probes immobilised on a matrix. The method is useful for
CC analysing nucleotide sequences in order to detect a genetic event such as
CC a SNP. The method is sensitive and specific for detecting the target
CC nucleotide sequence. The present sequence represents a fluorescent
CC donor/quencher-labelled protein kinase C (PKC) alpha substrate used in an
CC exemplification of the invention in the detection of thiol (SH)-labelled
CC oligonucleotides. The SH-labelled oligonucleotide is contacted with PKC-
CC alpha, and a disulphide bond is allowed to form between the
CC oligonucleotide and the PKC-alpha. The activity of the PKC-alpha is then
CC detected using this sequence

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3
|||
Db 1 ARK 3

RESULT 66

AAY54479

ID AAY54479 standard; peptide; 11 AA.

XX

AC AAY54479;

XX

DT 25-APR-2000 (first entry)

XX

DE Peptide used to treat infections, inflammation and tumours.

XX

KW Polycationic peptide; infection; inflammation; tumour; lactoferrin;
KW lactoferricin; conalbumin; ovotransferrin; antimicrobial; synergist;
KW antibacterial; antiviral; antifungal; candidiasis; defensin; magainin;
KW cecropin; protegrin; indolicidin analogue; histone;
KW acquired immune deficiency syndrome.

XX

OS Unidentified.

XX

PN WO200000214-A2.

XX

PD 06-JAN-2000.

XX

PF 28-JUN-1999; 99WO-EP004067.

XX

PR 26-JUN-1998; 98NL-01009505.

PR 09-OCT-1998; 98NL-01010284.

PR 06-NOV-1998; 98EP-00203765.

XX

PA (NUTR-) NUTRICIA NV.

XX

PI Swart PJ, Kuipers ME, Meijer DKF, Hageman RJJ, Van Den Berg JJM;

XX

DR WPI; 2000-160640/14.

XX

PT Composition containing cationic protein or peptide and buffer, used to
PT treat or prevent infections, inflammation and tumors, e.g. Candida.
XX
PS Claim 3; Page 43; 90pp; English.
XX
CC AAY54468-95 represent exemplary polycationic peptides which are used in
CC medicaments for treating and preventing infections (by bacteria, fungi,
CC viruses), inflammation and tumors. For peptides AAY54483-86, a peptide
CC comprising one of these sequences is used. Polycationic peptides may be
CC derived from human or bovine lactoferrin (preferred), lactoferricin, or
CC conalbumin (ovotransferrin), as well as alpha or beta defensins,
CC magainins, cecropins type A or B, protegrins, indolicidin analogues, and
CC polycations isolatable from insects and histones. The medicament
CC comprises a buffer which maintains a preselected pH in treated tissue.
CC The buffer provides a tissue pH at which growth of Candida is reduced.
CC The peptides show a synergistic effect when combined with known
CC antimicrobials, so allow a reduction in the dose of such compounds. The
CC medicaments are used to treat and/or prevent infections, inflammation and
CC tumors, or when used with separately administered antibacterial,
CC antiviral or antifungal agents, to provide a synergistic effect,
CC especially for treating candidiasis, e.g. in patients with acquired
CC immune deficiency syndrome
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 1 KSR 3

RESULT 67
AAB29416
ID AAB29416 standard; peptide; 11 AA.
XX
AC AAB29416;
XX
DT 09-FEB-2001 (first entry)
XX
DE Synthetic transduction domain, SEQ ID NO:3.
XX
KW Protein transduction domain; fusion molecule; therapeutic agent;
KW drug targetting; drug discovery; cell transduction; bioavailability;
KW vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;
KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;
KW spongiform encephalopathy; dyslexia; age-related memory loss;
KW Lou Gehring's disease; viral infection; HIV; bacterial infection.
XX
OS Synthetic.
XX
PN WO200062067-A1.
XX
PD 19-OCT-2000.

XX
PF 28-FEB-2000; 2000WO-US005097.
XX
PR 28-FEB-1999; 99US-0122757P.
PR 29-AUG-1999; 99US-0151291P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Dowdy SF;
XX
DR WPI; 2000-647439/62.
XX
PT Fusion molecules comprising protein transduction domains and therapeutic agents, useful for treating e.g. Alzheimer's and Parkinson's diseases, dementia and epilepsy.
XX
PS Claim 36; Page 147; 191pp; English.
XX
CC The invention relates to a novel fusion molecule comprising at least one protein transduction domain (PTD) and at least one linked molecule, where the linked molecule has therapeutic or prophylactic activity against a medical condition. The invention also relates to methods of drug discovery in which the test compound is linked to a suitable transducing protein and introduced to a cell; a method of killing resistant microorganisms using a suitable fusion molecule; a mammal comprising a covalently linked fusion molecule; and a mammal adapted for experimental use in which at least one transduction molecule has been transduced into essentially all the cells of the mammal. The fusion molecule is used to deliver a therapeutic agent to a mammal, especially a human. The linked molecule may be a vaccine, an anti-infective drug, a cardiovascular drug, an antitumour drug, an analgesic, an antiinflammatory, a diagnostic marker or a drug for the treatment or prevention of a central or peripheral nervous system disorder. The central nervous system (CNS) disorder is especially Alzheimer's disease, Parkinson's disease, Huntington's disease, and also includes pre-senile dementia, epilepsy and seizures, compulsive behaviour, meningitis (including viral and bacterial meningitis), encephalitis, ischaemia, scrapie (or related spongiform encephalopathies), dyslexia, age-related memory loss or Lou Gehring's disease. Fusion molecules can also be used to kill virally infected cells, especially those infected with HIV. The vaccines are used to treat or prevent bacterial or viral infections. The methods are a highly effective means for transducing a molecule into an entire mammal or into specific cells, tissues, organs and systems within it. They also overcome bioavailability problems that are associated with many therapeutic agents (e.g., large molecular size, hydrophobicity, hydrophilicity, biological resistance), by providing efficient transduction of the target cell. The present sequence represents a specifically claimed protein transduction domain
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||

RESULT 68

AAB26504

ID AAB26504 standard; peptide; 11 AA.

XX

AC AAB26504;

XX

DT 11-JAN-2001 (first entry)

XX

DE Human IgE C epsilon4 domain epitope P8.

XX

KW IgE; C epsilon3; C epsilon4; histamine release inhibitor; vaccine;

KW antibody; epitope; mimotope; human.

XX

OS Homo sapiens.

XX

PN WO200050461-A1.

XX

PD 31-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-EP001456.

XX

PR 25-FEB-1999; 99GB-00004408.

PR 21-JUL-1999; 99GB-00017144.

PR 07-AUG-1999; 99GB-00018598.

PR 07-AUG-1999; 99GB-00018599.

PR 07-AUG-1999; 99GB-00018601.

PR 07-AUG-1999; 99GB-00018604.

PR 07-AUG-1999; 99GB-00018606.

PR 29-OCT-1999; 99GB-00025618.

XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX

PI Friede M, Mason S, Turnell WG, Van Mechelen MP;

PI Vinals Y De BassolsC;

XX

DR WPI; 2000-572074/53.

XX

PT Peptides comprising surface exposed epitopes or mimotopes derived from C-
PT epsilon-3 or C-epsilon-4 domains of IgE, useful for preventing or
PT treating allergy.

XX

PS 4; Page 4; 76pp; English.

XX

CC The present invention relates epitopes and mimotopes of an isolated
CC surface exposed epitope of C epsilon3 or C epsilon4 domain of IgE. The
CC epitopes were identified by calculating the accessible surface of each
CC IgE residue. Mimotopes were designed to be similar to the epitopes. The
CC epitopes are useful in preparing medicaments for treating or preventing
CC allergies. The epitopes and mimotopes of the invention induce anti-IgE
CC antibodies which are capable of raising non-anaphylactic antibodies and
CC inhibiting histamine release. The present sequence is an IgE C epsilon4
CC domain epitope

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 6 SRD 8

RESULT 69

AAB08569

ID AAB08569 standard; peptide; 11 AA.

XX

AC AAB08569;

XX

DT 20-DEC-2000 (first entry)

XX

DE Peptide identified from a databank of polypeptides and polynucleotides.

XX

KW Precursor peptide; polypeptide hormone; peptide identification.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "hydrogen attached"

FT Modified-site 11

FT /note= "amidated residue"

XX

PN WO200050636-A1.

XX

PD 31-AUG-2000.

XX

PF 24-FEB-2000; 2000WO-FR000460.

XX

PR 25-FEB-1999; 99US-00257525.

XX

PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Camara Y FerrerJA, Thurieau C, Martinez J, Berge G, Goze C;

XX

DR WPI; 2000-572101/53.

XX

PT Identifying peptide with selected function, useful particularly for C-
PT amidated hormones, by screening database for combination of nucleic acid
PT and amino acid sequences.

XX

PS Disclosure; Page 21; 40pp; French.

XX

CC The specification describes a method for identifying a peptide having a
CC particular function. The method comprises preparing a database of
CC polynucleotides and polypeptides of unknown functions, screening the
CC database for a combination of nucleotides or amino acids indicative of
CC the peptide with a particular function, and identifying polynucleotides

CC and proteins which contain the peptide. The method is used to identify
CC precursor peptides with an amidated C-terminus, especially polypeptide
CC hormones, for studying physiologically active substances. The present
CC sequence represents a peptide which was identified using the method of
CC the invention

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 6 DMT 8

RESULT 70

AAB08606

ID AAB08606 standard; peptide; 11 AA.

XX

AC AAB08606;

XX

DT 20-DEC-2000 (first entry)

XX

DE Peptide identified from an origin of spliceosome associated protein 114.

XX

KW Precursor peptide; polypeptide hormone; peptide identification.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "hydrogen attached"
FT Modified-site 11
FT /note= "amidated residue"

XX

PN WO200050636-A1.

XX

PD 31-AUG-2000.

XX

PF 24-FEB-2000; 2000WO-FR000460.

XX

PR 25-FEB-1999; 99US-00257525.

XX

PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Camara Y FerrerJA, Thurieau C, Martinez J, Berge G, Goze C;

XX

DR WPI; 2000-572101/53.

XX

PT Identifying peptide with selected function, useful particularly for C-
PT amidated hormones, by screening database for combination of nucleic acid
PT and amino acid sequences.

XX

PS Disclosure; Page 22; 40pp; French.

XX
CC The specification describes a method for identifying a peptide having a particular function. The method comprises preparing a database of polynucleotides and polypeptides of unknown functions, screening the database for a combination of nucleotides or amino acids indicative of the peptide with a particular function, and identifying polynucleotides and proteins which contain the peptide. The method is used to identify precursor peptides with an amidated C-terminus, especially polypeptide hormones, for studying physiologically active substances. The present sequence represents a peptide which was identified using the method of the invention
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10
|||
Db 9 TAI 11

RESULT 71
AAG65304
ID AAG65304 standard; protein; 11 AA.
XX
AC AAG65304;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain CDR3 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004170.
XX
PR 10-FEB-2000; 2000US-0181608P.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human interleukin-18
PT useful for treating, e.g., inflammatory disorders, neurological

PT disorders, heart failure, myocardial infarction, and autoimmune diseases.

XX

PS Claim 27; Page 38; 91pp; English.

XX

CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain CDR3 fragment

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6

|||

Db 2 SRD 4

RESULT 72

AAB55201

ID AAB55201 standard; peptide; 11 AA.

XX

AC AAB55201;

XX

DT 05-MAR-2001 (first entry)

XX

DE Anti-RSV F1 DP178 region amino truncation peptide #8.

XX

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW antifusogenic; mobile blood component; measles virus; MeV; SIV;
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX

OS Human respiratory syncytial virus.

XX

PN WO200069902-A1.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013651.

XX

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX
DR WPI; 2001-007496/01.
XX
PT A modified peptide and a reactive group which is reactive with amino
PT groups, hydroxyl groups, or thiol groups on blood components to form
PT stable covalent bonds useful for treatment of viral infections, e.g.
PT human immunodeficiency virus.
XX
PS Disclosure; Page 150; 211pp; English.
XX
CC The present invention describes a modified anti-viral peptide (I)
CC comprising a peptide that exhibits anti-viral activity and a reactive
CC group which is reactive with amino groups, hydroxyl groups, or thiol
CC groups on blood components to form stable covalent bonds. (I) has anti-
CC viral and anti-fusogenic activities. (I) inhibits viral infection of
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
CC the level of membrane fusion events between two or more entities, e.g.,
CC virus-cell or cell-cell, relative to the level of membrane fusion that
CC occurs in the absence of the peptide. (I) is useful in the treatment of
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
CC MeV, and SIV. (I) may be administered prophylactically to previously
CC uninfected individuals. This is useful in cases where an individual has
CC been subjected to a high risk of exposure to a virus. By bonding of long-
CC lived components of the blood, such as immunoglobin, serum albumin, red
CC blood cells and platelets the activity is extended for days to weeks.
CC This is due to improved stability in vivo and a reduced susceptibility to
CC peptidase or protease degradation. This minimises the need for more
CC frequent, or even continual, administration of the peptides. AAB54784 to
CC AAB55431 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 5 RKS 7

RESULT 73
AAE05275
ID AAE05275 standard; peptide; 11 AA.
XX
AC AAE05275;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human immunodeficiency virus (HIV) TAT mutant peptide #2.
XX
KW DNA recombinase domain; protein transduction domain; PTD; mutant;

KW gene alteration; TAT protein; mutein; Human immunodeficiency virus; HIV.
XX
OS Human immunodeficiency virus.
OS Synthetic.
XX
PN WO200149832-A2.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-EP000060.
XX
PR 07-JAN-2000; 2000EP-00100351.
PR 10-NOV-2000; 2000EP-00124595.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Schwenk F;
XX
DR WPI; 2001-441873/47.
XX
PT Using site-specific DNA recombinase domain/protein transduction domain
PT fusion proteins for inducing target gene alterations in organisms or cell
PT cultures.
XX
PS Claim 5; Page 71; 85pp; English.
XX
CC The present invention relates to use of fusion proteins comprising a site
CC -specific DNA recombinase domain e.g. Cre and a protein transduction
CC domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT
CC peptide, for preparing an agent for inducing target gene alterations in a
CC living organism or cell culture. The present invention also provides a
CC method for inducing gene alterations in living organisms using the fusion
CC proteins of the invention. The present sequence is a HIV TAT mutant
CC peptide
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 74
AAG99815
ID AAG99815 standard; peptide; 11 AA.
XX
AC AAG99815;
XX
DT 27-SEP-2001 (first entry)
XX
DE ERA binding domain polypeptide SEQ ID NO 257.
XX
KW ERA binding domain; Escherichia coli; GTPase; antimicrobial;

KW antibacterial; antibiotic; pathogenesis; infection; vaccine;
KW peptide therapy.
XX
OS Schizosaccharomyces pombe.
XX
PN WO200153458-A2.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-US001786.
XX
PR 18-JAN-2000; 2000US-0176870P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Lupas AN, Pearce KH;
XX
DR WPI; 2001-476108/51.
XX
PT New ERA binding domain polypeptides and polynucleotides encoding them,
PT useful as research reagents and materials for discovery of treatments and
PT diagnostics for diseases, or for genetic immunization.
XX
PS Claim 1; Page 36; 279pp; English.
XX
CC The present invention relates to ERA binding domain polypeptides
CC (AAG99559-AAG99989 and AAM00010-AAM00021). The era gene in Escherichia
CC coli codes for an essential GTPase protein able to autophosphorylate at
CC serine and/or threonine residues. The protein has potential antimicrobial
CC and antibacterial activity and is useful in screening for antagonists,
CC agonists and for compounds with antibiotic activity. The proteins are
CC also useful in determining their role in pathogenesis of infection,
CC dysfunction and disease and could be used as part of a vaccine and/or
CC peptide therapy
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 7 ARK 9

RESULT 75
ABB59308
ID ABB59308 standard; protein; 11 AA.
XX
AC ABB59308;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 4716.
XX

KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL03411.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
XX
PS Disclosure; SEQ ID NO 4716; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://ftp.wipo.int/pub/published_pct_sequences)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9
|||
Db 1 MTA 3

Search completed: April 8, 2004, 15:40:13
Job time : 44.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
(without alignments)
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Title: US-09-787-443A-22

Perfect score: 11

Sequence: 1 ARKS RDM TAIK 11

Scoring table: OLIGO
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Searched: 389414 seqs, 51625971 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

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1		4	36.4	11	1	US-08-185-448-5		Sequence 5, Appli
2		4	36.4	11	2	US-08-747-137-63		Sequence 63, Appl
3		4	36.4	11	3	US-08-696-854B-3		Sequence 3, Appli
4		4	36.4	11	4	US-09-576-824A-547		Sequence 547, App
5		4	36.4	11	4	US-09-576-824A-548		Sequence 548, App
6		4	36.4	11	4	US-09-576-824A-549		Sequence 549, App
7		4	36.4	11	5	PCT-US91-08328-13		Sequence 13, Appl
8		3	27.3	11	1	US-07-851-941-12		Sequence 12, Appl
9		3	27.3	11	1	US-08-197-795-5		Sequence 5, Appli
10		3	27.3	11	1	US-08-431-539-10		Sequence 10, Appl
11		3	27.3	11	1	US-08-431-539-16		Sequence 16, Appl

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13	3	27.3	11	2	US-08-456-670B-28	Sequence 28, Appl
14	3	27.3	11	2	US-08-350-260A-340	Sequence 340, App
15	3	27.3	11	2	US-08-350-260A-342	Sequence 342, App
16	3	27.3	11	2	US-08-350-260A-349	Sequence 349, App
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20	3	27.3	11	2	US-08-350-260A-430	Sequence 430, App
21	3	27.3	11	2	US-08-350-260A-516	Sequence 516, App
22	3	27.3	11	2	US-08-350-260A-522	Sequence 522, App
23	3	27.3	11	2	US-08-751-767A-29	Sequence 29, Appl
24	3	27.3	11	2	US-09-115-209-74	Sequence 74, Appl
25	3	27.3	11	3	US-08-817-926-6	Sequence 6, Appli
26	3	27.3	11	3	US-08-746-160-51	Sequence 51, Appl
27	3	27.3	11	3	US-08-810-324-46	Sequence 46, Appl
28	3	27.3	11	3	US-08-679-006-16	Sequence 16, Appl
29	3	27.3	11	3	US-09-183-217-9	Sequence 9, Appli
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39	3	27.3	11	3	US-09-410-025-3	Sequence 3, Appli
40	3	27.3	11	3	US-09-410-025-4	Sequence 4, Appli
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43	3	27.3	11	3	US-09-410-025-7	Sequence 7, Appli
44	3	27.3	11	3	US-09-410-025-8	Sequence 8, Appli
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47	3	27.3	11	4	US-09-025-769B-186	Sequence 186, App
48	3	27.3	11	4	US-09-227-357-567	Sequence 567, App
49	3	27.3	11	4	US-09-314-268-171	Sequence 171, App
50	3	27.3	11	4	US-09-277-599B-2	Sequence 2, Appli
51	3	27.3	11	4	US-09-149-476-698	Sequence 698, App
52	3	27.3	11	4	US-09-177-165A-1	Sequence 1, Appli
53	3	27.3	11	4	US-08-255-208A-77	Sequence 77, App
54	3	27.3	11	4	US-08-469-260A-550	Sequence 550, App
55	3	27.3	11	4	US-09-561-490E-56	Sequence 56, App
56	3	27.3	11	4	US-09-104-337A-340	Sequence 340, App
57	3	27.3	11	4	US-09-104-337A-342	Sequence 342, App
58	3	27.3	11	4	US-09-104-337A-349	Sequence 349, App
59	3	27.3	11	4	US-09-104-337A-375	Sequence 375, App
60	3	27.3	11	4	US-09-104-337A-424	Sequence 424, App
61	3	27.3	11	4	US-09-104-337A-427	Sequence 427, App
62	3	27.3	11	4	US-09-104-337A-430	Sequence 430, App
63	3	27.3	11	4	US-09-104-337A-516	Sequence 516, App
64	3	27.3	11	4	US-09-104-337A-522	Sequence 522, App
65	3	27.3	11	4	US-09-810-873-2	Sequence 2, Appli
66	3	27.3	11	4	US-08-488-446-550	Sequence 550, App
67	3	27.3	11	4	US-08-467-344A-550	Sequence 550, App
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72	3	27.3	11	4	US-08-475-955-56	Sequence 56, Appl
73	3	27.3	11	4	US-09-775-052A-3	Sequence 3, Appli
74	3	27.3	11	4	US-09-576-824A-482	Sequence 482, App
75	3	27.3	11	4	US-09-576-824A-546	Sequence 546, App
76	3	27.3	11	5	PCT-US95-01721-5	Sequence 5, Appli
77	3	27.3	11	6	5187155-26	Patent No. 5187155
78	2	18.2	11	1	US-09-572-339-11	Sequence 11, Appl
79	2	18.2	11	1	US-07-596-081A-29	Sequence 29, Appl
80	2	18.2	11	1	US-07-696-551B-10	Sequence 10, Appl
81	2	18.2	11	1	US-07-666-719-20	Sequence 20, Appl
82	2	18.2	11	1	US-07-763-512-4	Sequence 4, Appli
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95	2	18.2	11	1	US-07-699-468-3	Sequence 3, Appli
96	2	18.2	11	1	US-07-699-468-7	Sequence 7, Appli
97	2	18.2	11	1	US-08-049-871-6	Sequence 6, Appli
98	2	18.2	11	1	US-08-049-871-8	Sequence 8, Appli
99	2	18.2	11	1	US-07-672-483-17	Sequence 17, Appl
100	2	18.2	11	1	US-07-791-935B-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-08-185-448-5

; Sequence 5, Application US/08185448
; Patent No. 5580747
; GENERAL INFORMATION:
; APPLICANT: SHULTZ, JOHN W.
; APPLICANT: WHITE, DOUGLAS H.
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,448
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,928
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SARA, CHARLES S
; REGISTRATION NUMBER: 30492
; REFERENCE/DOCKET NUMBER: F.3347-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 255-2022
; TELEFAX: (608) 255-2182
; TELEX: 26832 ANDSTARK
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1
; OTHER INFORMATION: /label= LABEL
; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE"
; OTHER INFORMATION: DETECTION TAG"
US-08-185-448-5

Query Match 36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
|||
Db 5 RKS 8

RESULT 2
US-08-747-137-63
; Sequence 63, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
US-08-747-137-63

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
|||
Db 5 RKS 8

RESULT 3
US-08-696-854B-3
; Sequence 3, Application US/08696854B
; Patent No. 6017878
; GENERAL INFORMATION:
; APPLICANT: SARAGOVI, Uri H.
; APPLICANT: LeSAUTEUR, Lynne
; APPLICANT: CUELLO, Claudio A.
; TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
; TITLE OF INVENTION: AND THEIR USES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON

; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,854B
; FILING DATE: 07-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA95/00059
; FILING DATE: 07-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9402331.4
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 487-5800
; TELEFAX: (201) 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: one-of (1, 11)
; OTHER INFORMATION: /note= "Xaa is any uncharged amino acid
; OTHER INFORMATION: or hydrophobic amino acid"
US-08-696-854B-3

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAIK 11
|||
Db 3 TAIK 6

RESULT 4
US-09-576-824A-547
; Sequence 547, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPEs, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 547
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involving these two groups
US-09-576-824A-547

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
Db 7 RKS 10

RESULT 5

US-09-576-824A-548

; Sequence 548, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPEs AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPEs, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM

; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involving these two groups
US-09-576-824A-548

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
| | | |
Db 6 RKS 9

RESULT 6
US-09-576-824A-549
; Sequence 549, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30

; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 549
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involving these two groups
US-09-576-824A-549

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 5
|||
Db 5 RKS 8

RESULT 7

PCT-US91-08328-13

; Sequence 13, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08328

;
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 6..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val sequence"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-13

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKSR 5
 ||||
Db 5 RKSR 8

RESULT 8
US-07-851-941-12
; Sequence 12, Application US/07851941
; Patent No. 5428016
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

;
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/851,941
; FILING DATE: 19920313
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/851,941
; FILING DATE: March 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:

; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-851-941-12

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 1 KSR 3

RESULT 9

US-08-197-795-5

; Sequence 5, Application US/08197795
; Patent No. 5457182
; GENERAL INFORMATION:
; APPLICANT: Wiederrecht, Gregory J.
; APPLICANT: Sewell, Tonya J.
; TITLE OF INVENTION: FK-506 CYTOSOLIC BINDING PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,795
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Thies, J. Eric
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-197-795-5

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 10

US-08-431-539-10

;
; Sequence 10, Application US/08431539
;
; Patent No. 5580751
;
; GENERAL INFORMATION:
;
; APPLICANT: Buchardt, Ole
;
; APPLICANT: Breddam, Klaus
;
; APPLICANT: Henriksen, Dennis
;
; TITLE OF INVENTION: Process for the Preparation of
;
; TITLE OF INVENTION: C-Terminally Amidated Peptides
;
; NUMBER OF SEQUENCES: 19
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Merchant & Gould
;
; STREET: 3100 No. 5580751west Center
;
; CITY: Minneapolis
;
; STATE: MN
;
; COUNTRY: USA
;
; ZIP: 55402
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/431,539
;
; FILING DATE:
;
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/039,306
;
; FILING DATE: 15-APR-1993
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Nelson, Albin J.
;
; REGISTRATION NUMBER: 28,650
;
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 612-332-5300
;
; TELEFAX: 612-332-9081
;
; INFORMATION FOR SEQ ID NO: 10:
;
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-431-539-10

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10
|||
Db 3 TAI 5

RESULT 11

US-08-431-539-16

; Sequence 16, Application US/08431539
; Patent No. 5580751
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Breddam, Klaus
; APPLICANT: Henriksen, Dennis
; TITLE OF INVENTION: Process for the Preparation of
; TITLE OF INVENTION: C-Terminally Amidated Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5580751west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,539
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,306
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-431-539-16

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10
|||
Db 3 TAI 5

RESULT 12

US-08-615-181-84

; Sequence 84, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,181
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01756
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 261302/1993
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-84

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 7 RKS 9

RESULT 13

US-08-456-670B-28

; Sequence 28, Application US/08456670B
; Patent No. 5932415

; GENERAL INFORMATION:

; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAWEZIK, MARTINA
; APPLICANT: LINXWEILER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN

; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: DE 4239567.4

;

FILING DATE: 25-NOV-1992

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: DE 4219111.4

;

FILING DATE: 11-JUN-1992

;

ATTORNEY/AGENT INFORMATION:

;

NAME: HAMLET-KING, DIANA

;

REGISTRATION NUMBER: 33,302

;

REFERENCE/DOCKET NUMBER: MERCK 1694D1

;

TELECOMMUNICATION INFORMATION:

;

TELEPHONE: 703-243-6333

;

TELEFAX: 703-243-6410

;

TELEX: 64191

;

INFORMATION FOR SEQ ID NO: 28:

;

SEQUENCE CHARACTERISTICS:

;

LENGTH: 11 amino acids

;

TYPE: amino acid

;

TOPOLOGY: linear

;

MOLECULE TYPE: peptide

;

ORIGINAL SOURCE:

;

ORGANISM: Listeria monocytogenes

;

STRAIN: EGD

US-08-456-670B-28

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 2 AIK 4

RESULT 14

US-08-350-260A-340

;

Sequence 340, Application US/08350260A

;

Patent No. 5962255

;

GENERAL INFORMATION:

;

APPLICANT: Winter, Gregory Paul

;

APPLICANT: Griffiths, Andrew David

;

APPLICANT: Williams, Samuel Cameron

;

APPLICANT: Waterhouse, Peter

;

APPLICANT: Nissim, Ahuva

;

APPLICANT: Johnson, Kevin Stuart

;

APPLICANT: Smith, Andrew John Hammond

;

TITLE OF INVENTION: Methods for producing members of specific

;

TITLE OF INVENTION: binding pairs

;

NUMBER OF SEQUENCES: 602

;

CORRESPONDENCE ADDRESS:

;

ADDRESSEE: David W. Clough

;

STREET: Marshall, O'Toole, Gerstein, Murray & Borun

;

STREET: 6300 Sears Tower, 233 South Wacker Drive

;

CITY: Chicago

;

STATE: Illinois

;

COUNTRY: USA

;

ZIP: 60606-6402

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 340:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-340

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 15
US-08-350-260A-342
; Sequence 342, Application US/08350260A
; Patent No. 5962255

; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 342:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-342

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 16

US-08-350-260A-349

; Sequence 349, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-350-260A-349

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 17

US-08-350-260A-375

Sequence 375, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-375

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6
|||
Db 2 SRD 4

RESULT 18
US-08-350-260A-424
; Sequence 424, Application US/08350260A
; Patent No. 5962255

; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 424:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-424

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 19

US-08-350-260A-427

;
; Sequence 427, Application US/08350260A
; Patent No. 5962255
;
; GENERAL INFORMATION:
;
; APPLICANT: Winter, Gregory Paul
;
; APPLICANT: Griffiths, Andrew David
;
; APPLICANT: Williams, Samuel Cameron
;
; APPLICANT: Waterhouse, Peter
;
; APPLICANT: Nissim, Ahuva
;
; APPLICANT: Johnson, Kevin Stuart
;
; APPLICANT: Smith, Andrew John Hammond
;
; TITLE OF INVENTION: Methods for producing members of specific
;
; TITLE OF INVENTION: binding pairs
;
; NUMBER OF SEQUENCES: 602
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: David W. Clough
;
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
;
; STREET: 6300 Sears Tower, 233 South Wacker Drive
;
; CITY: Chicago
;
; STATE: Illinois
;
; COUNTRY: USA
;
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/350,260A
;
; FILING DATE: 05-DEC-1994
;
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: GB 9110549.4
;
; FILING DATE: 15-MAY-1991
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: GB 9206318.9
;
; FILING DATE: 24-MAR-1992
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/GB91/01134
;
; FILING DATE: 10-JUL-1991
;
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 427:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-350-260A-427

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 20
US-08-350-260A-430
Sequence 430, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
;
; INFORMATION FOR SEQ ID NO: 430:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-430

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 21
US-08-350-260A-516
; Sequence 516, Application US/08350260A
; Patent No. 5962255

; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 516:
; SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-516

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 22

US-08-350-260A-522

; Sequence 522, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 522:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-522

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6
|||
Db 2 SRD 4

RESULT 23
US-08-751-767A-29
; Sequence 29, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-751-767A-29

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 2 RKS 4

RESULT 24

US-09-115-209-74

Sequence 74, Application US/09115209
Patent No. 5998375
GENERAL INFORMATION:
APPLICANT: Thogersen, Henning
APPLICANT: Madsen, Kjeld
APPLICANT: Olsen, Uffe B.
APPLICANT: Johansen, Nils L.
APPLICANT: Scheideler, Mark
TITLE OF INVENTION: No. 5998375iceptin Analogues
FILE REFERENCE: 5285.200-US
CURRENT APPLICATION NUMBER: US/09/115,209
CURRENT FILING DATE: 1998-07-14
EARLIER APPLICATION NUMBER: 0867/97
EARLIER FILING DATE: 1997-07-15
EARLIER APPLICATION NUMBER: 60/052,862
EARLIER FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 74
LENGTH: 11
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: Xaa at position 10 is Orn

US-09-115-209-74

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 7 ARK 9

RESULT 25

US-08-817-926-6

; Sequence 6, Application US/08817926

; Patent No. 6001590

; GENERAL INFORMATION:

; APPLICANT: Komeda, Toshihiro

; APPLICANT: Suda, Hisako

; APPLICANT: Tamai, Yukio

; APPLICANT: Iwamatsu, Akihiro

; APPLICANT: Kato, No. 6001590uo

; APPLICANT: Sakai, Yasuyoshi

; TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINII

; TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,926

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP96/02597

; FILING DATE: 12-SEP-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 234133/1995

; FILING DATE: 12-SEP-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 42536/1996

; FILING DATE: 29-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 081356/0112

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-817-926-6

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RDM 7
|||
Db 6 RDM 8

RESULT 26

US-08-746-160-51

; Sequence 51, Application US/08746160
; Patent No. 6010876
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia L.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Lee, In-Hee
; TITLE OF INVENTION: CLAVANINS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,160
; FILING DATE: 06-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20563.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-746-160-51

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 5 RKS 7

RESULT 27

US-08-810-324-46

; Sequence 46, Application US/08810324C
; Patent No. 6040293
; GENERAL INFORMATION:
; APPLICANT: LEHRER, Robert I
; APPLICANT: ZHAO, Chengquan
; APPLICANT: LEE, In-Hee
; APPLICANT: HARWIG, Sylvia L.
; TITLE OF INVENTION: CLAVANINS
; FILE REFERENCE: 22000-20563.20
; CURRENT APPLICATION NUMBER: US/08/810,324C
; CURRENT FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: 08/746,160
; EARLIER FILING DATE: 1996-11-06
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Styela clava
US-08-810-324-46

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 5 RKS 7

RESULT 28

US-08-679-006-16

; Sequence 16, Application US/08679006
; Patent No. 6150500
; GENERAL INFORMATION:
; APPLICANT: Salerno, John C.
; TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF
; TITLE OF INVENTION: NOS ISOFORMS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

;
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,006
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: JCS96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-679-006-16

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 4 RKS 6

RESULT 29

US-09-183-217-9

;
; Sequence 9, Application US/09183217A
; Patent No. 6153194
; GENERAL INFORMATION:
; APPLICANT: Skare, Jonathan T.
; APPLICANT: Shang, Ellen S.
; APPLICANT: Champion, Cheryl I.
; APPLICANT: Blanco, David R.
; APPLICANT: Miller, James N.
; APPLICANT: Lovett, Michael A.
; APPLICANT: Mizabekov, Tajib A.
; APPLICANT: Kagan, Bruce L.
; APPLICANT: Tempst, Paul
; APPLICANT: Foley, Denise M.
; TITLE OF INVENTION: BORRELIA BURGDORFERI OUTER MEMBRANE PROTEINS
; FILE REFERENCE: UC Case No. 6153194 96-059-3/Skare et al.
; CURRENT APPLICATION NUMBER: US/09/183,217A
; CURRENT FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: 08/787,367
; PRIOR FILING DATE: 1997-01-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-183-217-9

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 9 AIK 11

RESULT 30

US-09-206-059-4

; Sequence 4, Application US/09206059
; Patent No. 6201104
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
; TITLE OF INVENTION: Proteins and Methods of Use
; FILE REFERENCE: 05213-0370
; CURRENT APPLICATION NUMBER: US/09/206,059
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding peptides
US-09-206-059-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 5 AIK 7

RESULT 31

US-09-208-966-3

; Sequence 3, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.

; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 32

US-08-647-405B-3

; Sequence 3, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 3 ARK 5

RESULT 33
US-08-647-405B-4
; Sequence 4, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 3 ARK 5

RESULT 34
US-09-177-249-212
; Sequence 212, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Arabidopsis sp.
US-09-177-249-212

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 2 RKS 4

RESULT 35

US-09-248-588-70

; Sequence 70, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

US-09-248-588-70

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 8 SRD 10

RESULT 36

US-08-160-604-73

; Sequence 73, Application US/08160604
; Patent No. 6232522
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; APPLICANT: James, Judith A.
; APPLICANT: Scofield, R. H.
; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL
SYMPTOMATOLOGY
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta

;
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,604
; FILING DATE: 30-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,819
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,205
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-160-604-73

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9
|||
Db 9 MTA 11

RESULT 37
US-09-410-025-1
; Sequence 1, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-1

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 38
US-09-410-025-2
; Sequence 2, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-2

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 39

US-09-410-025-3

; Sequence 3, Application US/09410025

; Patent No. 6251623

; GENERAL INFORMATION:

; APPLICANT: ARAHIRA, MASAOMI

; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED, ASPARAGINE

; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE

; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: JP10-327536

; PRIOR FILING DATE: 1998-11-04

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Glycine max

US-09-410-025-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5

|||

Db 2 KSR 4

RESULT 40

US-09-410-025-4

; Sequence 4, Application US/09410025

; Patent No. 6251623

; GENERAL INFORMATION:

; APPLICANT: ARAHIRA, MASAOMI

; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED, ASPARAGINE

; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE

; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: JP10-327536

; PRIOR FILING DATE: 1998-11-04

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Glycine max

US-09-410-025-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 41

US-09-410-025-5

; Sequence 5, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max

US-09-410-025-5

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 42

US-09-410-025-6

; Sequence 6, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-6

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 43

US-09-410-025-7

; Sequence 7, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-7

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 44

US-09-410-025-8

; Sequence 8, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-8

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 45

US-09-410-025-9

; Sequence 9, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-9

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 46

US-09-410-025-10

; Sequence 10, Application US/09410025
; Patent No. 6251623

; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-10

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 2 KSR 4

RESULT 47
US-09-025-769B-186
; Sequence 186, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-025-769B-186

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10
|||
Db 4 TAI 6

RESULT 48

US-09-227-357-567

; Sequence 567, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916

; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 567
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-227-357-567

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 49

US-09-314-268-171

; Sequence 171, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
; TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/314,268
; EARLIER FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-09-314-268-171

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 50

US-09-277-599B-2

; Sequence 2, Application US/09277599B
; Patent No. 6395879
; GENERAL INFORMATION:
; APPLICANT: Mandrell, David
; APPLICANT: Bates, Anna
; APPLICANT: Brandon, David
; TITLE OF INVENTION: Monoclonal Antibodies Against Campylobacter jejuni and Campylobacter coli
; TITLE OF INVENTION: Outer Membrane Antigens
; FILE REFERENCE: Mandrell
; CURRENT APPLICATION NUMBER: US/09/277,599B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/080,166
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: The undetermined amino acid may or may not exist
US-09-277-599B-2

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 51

US-09-149-476-698

; Sequence 698, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585

;
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 AIK 6

RESULT 52

US-09-177-165A-1

; Sequence 1, Application US/09177165A
; Patent No. 6426205
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/09/177,165A
; CURRENT FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*

US-09-177-165A-1

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10

|||

Db 4 TAI 6

RESULT 53

US-08-255-208A-77

; Sequence 77, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= A
; OTHER INFORMATION: /note= "Preceeding this amino acid, there may be an
amino group
; OTHER INFORMATION: an acetyl group, a 9-fluorenylmethoxy-carbonyl group,
a hydroph
; OTHER INFORMATION: group or a macromolecular carrier group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /label= B
; OTHER INFORMATION: /note= "Following this amino acid, there may be a
carboxyl grou
; OTHER INFORMATION: an amido group, a hydrophobic group, or a
macromolecular carrie
; OTHER INFORMATION: group."
US-08-255-208A-77

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 5 RKS 7

RESULT 54
US-08-469-260A-550
; Sequence 550, Application US/08469260A

; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-550

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 2 AIK 4

RESULT 55
US-09-561-490E-56
; Sequence 56, Application US/09561490E
; Patent No. 6468537
; GENERAL INFORMATION:
; APPLICANT: DATTA, Syamal K
; APPLICANT: KALIYAPERUMAL, Arunan
; TITLE OF INVENTION: LOCALIZATION OF MAJOR PEPTIDE AUTOEPITOPES FOR NUCLEOSOME
SPECIF
; TITLE OF INVENTION: IC T CELLS OF SYSTEMIC LUPUS ERYTHEMATOSUS
; FILE REFERENCE: 290-13U1 (53662-5017
; CURRENT APPLICATION NUMBER: US/09/561,490E
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,448
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Histone fragment
US-09-561-490E-56

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 9 KSR 11

RESULT 56
US-09-104-337A-340
; Sequence 340, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

;

ZIP: 60606-6402

;

COMPUTER READABLE FORM:

;

MEDIUM TYPE: Floppy disk

;

COMPUTER: IBM PC compatible

;

OPERATING SYSTEM: PC-DOS/MS-DOS

;

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/09/104,337A

;

FILING DATE: 25-Jun-1998

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: US 08/350,260

;

FILING DATE: 05-DEC-1994

;

APPLICATION NUMBER: GB 9110549.4

;

FILING DATE: 15-MAY-1991

;

APPLICATION NUMBER: GB 9206318.9

;

FILING DATE: 24-MAR-1992

;

APPLICATION NUMBER: PCT/GB92/00883

;

FILING DATE: 15-MAY-1992

;

APPLICATION NUMBER: PCT/GB93/00605

;

FILING DATE: 24-MAR-1993

;

APPLICATION NUMBER: US 08/150,002

;

FILING DATE: 31-MAR-1994

;

APPLICATION NUMBER: US 08/307,619

;

FILING DATE: 16-SEP-1994

;

ATTORNEY/AGENT INFORMATION:

;

NAME: Bartnicki, Audrey L.

;

REGISTRATION NUMBER: 40,499

;

REFERENCE/DOCKET NUMBER: 28111/32372A

;

TELECOMMUNICATION INFORMATION:

;

TELEPHONE: 312-474-6300

;

INFORMATION FOR SEQ ID NO: 340:

;

SEQUENCE CHARACTERISTICS:

;

LENGTH: 11 amino acids

;

TYPE: amino acid

;

STRANDEDNESS: single

;

TOPOLOGY: linear

;

SEQUENCE DESCRIPTION: SEQ ID NO: 340:

US-09-104-337A-340

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 57
US-09-104-337A-342
;

Sequence 342, Application US/09104337A

;

Patent No. 6492160

;

GENERAL INFORMATION:

;

APPLICANT: Winter, Gregory Paul

;

Griffiths, Andrew David

;

Williams, Samuel Cameron

;

Waterhouse, Peter

;
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

;
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

;
; CURRENT APPLICATION DATA:

;
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998

;
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994

;
; ATTORNEY/AGENT INFORMATION:

;
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A

;
; TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: 312-474-6300

;
; INFORMATION FOR SEQ ID NO: 342:

;
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;
; SEQUENCE DESCRIPTION: SEQ ID NO: 342:

US-09-104-337A-342

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 58

US-09-104-337A-349

; Sequence 349, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 349:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 349:
US-09-104-337A-349

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
Db 2 SRD 4

RESULT 59
US-09-104-337A-375
; Sequence 375, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 375:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 375:
US-09-104-337A-375

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 60
US-09-104-337A-424
; Sequence 424, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 424:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 424:
US-09-104-337A-424

```

Query Match           27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.8e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy          4  SRD  6
           |||
Db          2  SRD  4

```

RESULT 61
US-09-104-337A-427
; Sequence 427, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs

NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 427:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 427:
US-09-104-337A-427

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 62

US-09-104-337A-430

; Sequence 430, Application US/09104337A
; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A

; FILING DATE: 25-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/350,260

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: GB 9110549.4

; FILING DATE: 15-MAY-1991

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; APPLICATION NUMBER: PCT/GB92/00883

; FILING DATE: 15-MAY-1992

; APPLICATION NUMBER: PCT/GB93/00605

; FILING DATE: 24-MAR-1993

; APPLICATION NUMBER: US 08/150,002

; FILING DATE: 31-MAR-1994

; APPLICATION NUMBER: US 08/307,619

; FILING DATE: 16-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bartnicki, Audrey L.

; REGISTRATION NUMBER: 40,499

; REFERENCE/DOCKET NUMBER: 28111/32372A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 430:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 430:
US-09-104-337A-430

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 63

US-09-104-337A-516

; Sequence 516, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 516:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 516:
US-09-104-337A-516

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 64
US-09-104-337A-522
Sequence 522, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 522:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 522:

US-09-104-337A-522

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 65
US-09-810-873-2
; Sequence 2, Application US/09810873
; Patent No. 6551599
; GENERAL INFORMATION:
; APPLICANT: Mandrell, David
; APPLICANT: Bates, Anna
; APPLICANT: Brandon, David
; TITLE OF INVENTION: Monoclonal Antibodies Against Campylobacter jejuni and
Campylobacter coli
; TITLE OF INVENTION: Outer Membrane Antigens
; FILE REFERENCE: Mandrell
; CURRENT APPLICATION NUMBER: US/09/810,873
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/277,599
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2

; LENGTH: 11
; TYPE: PRT
; ORGANISM: *Campylobacter jejuni*
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()...()
; OTHER INFORMATION: The undetermined amino acid may or may not exist
US-09-810-873-2

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 66

US-08-488-446-550

; Sequence 550, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.

;
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-446-550

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 2 AIK 4

RESULT 67
US-08-467-344A-550
; Sequence 550, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 550:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-08-467-344A-550

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 2 AIK 4

RESULT 68
US-09-079-030-55
Sequence 55, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363

; REFERENCE/DOCKET NUMBER: ARAG:003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-55

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 4 AIK 6

RESULT 69

US-09-591-694-38

; Sequence 38, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related
Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-38

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 2 AIK 4

RESULT 70

US-09-535-852-1119

; Sequence 1119, Application US/09535852
; Patent No. 6638911

; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1119
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-09-535-852-1119

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 9 ARK 11

RESULT 71
US-09-535-852-1159
; Sequence 1159, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1159
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-09-535-852-1159

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 9 ARK 11

RESULT 72
US-08-475-955-56
; Sequence 56, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; TITLE OF INVENTION: AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8

US-08-475-955-56

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9
|||
Db 9 MTA 11

RESULT 73

US-09-775-052A-3

; Sequence 3, Application US/09775052A
; Patent No. 6645501
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human

US-09-775-052A-3

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 74

US-09-576-824A-482

; Sequence 482, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPEs AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPEs, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A

; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 482
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involving these two groups
US-09-576-824A-482

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 1 ARK 3

RESULT 75

US-09-576-824A-546

; Sequence 546, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22

; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 546
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involving these two groups
US-09-576-824A-546

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 8 RKS 10

Search completed: April 8, 2004, 15:52:17
Job time : 12.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
(without alignments)
122.816 Million cell updates/sec

Title: US-09-787-443A-22

Perfect score: 11

Sequence: 1 ARKS RD MTAIK 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	3	27.3	11	2	PH0919	T-cell receptor be
2	2	18.2	11	2	S32575	ribosomal protein
3	2	18.2	11	2	A40693	transgelin - sheep
4	2	18.2	11	2	A38841	rhodopsin homolog
5	2	18.2	11	2	A26930	ermG leader peptid
6	2	18.2	11	2	B26744	megascoliakinin -
7	2	18.2	11	2	JQ0395	hypothetical prote
8	2	18.2	11	2	S66606	quinoline 2-oxidor
9	2	18.2	11	2	S58244	pyrroloquinoline q
10	2	18.2	11	2	E60691	phycobilisome 8K 1
11	2	18.2	11	2	PC2372	58K heat shock pro
12	2	18.2	11	2	A44755	20alpha-hydroxyste
13	2	18.2	11	2	S33519	probable secreted

14	2	18.2	11	2	G61497	seed protein ws-23
15	2	18.2	11	2	PC4267	ribosomal protein
16	2	18.2	11	2	A38590	transforming prote
17	2	18.2	11	2	A34135	DNA-binding protei
18	2	18.2	11	2	A61512	variant surface gl
19	2	18.2	11	2	S05002	corazonin - Americ
20	2	18.2	11	2	S65395	chemical-sense-rel
21	2	18.2	11	2	E57789	gallbladder stone
22	2	18.2	11	2	S21727	gamma-interferon-i
23	2	18.2	11	2	PT0249	Ig heavy chain CRD
24	2	18.2	11	2	PT0273	Ig heavy chain CRD
25	2	18.2	11	2	S13279	Ile-Ser-bradykinin
26	2	18.2	11	2	S68637	acetylcholinestera
27	2	18.2	11	2	S54347	tubulin beta chain
28	2	18.2	11	2	PH1632	Ig H chain V-D-J r
29	2	18.2	11	2	PH1600	Ig H chain V-D-J r
30	2	18.2	11	2	PH1583	Ig H chain V-D-J r
31	2	18.2	11	2	PH1584	Ig H chain V-D-J r
32	2	18.2	11	2	PT0217	T-cell receptor be
33	2	18.2	11	2	PT0214	T-cell receptor be
34	2	18.2	11	2	C38887	T-cell receptor ga
35	2	18.2	11	2	PD0441	translation elonga
36	2	18.2	11	2	PH0929	T-cell receptor be
37	2	18.2	11	2	PH0947	T-cell receptor be
38	2	18.2	11	2	T12264	cytochrome-c oxida
39	2	18.2	11	2	T12253	cytochrome-c oxida
40	2	18.2	11	2	T12244	cytochrome-c oxida
41	2	18.2	11	2	T12248	cytochrome-c oxida
42	2	18.2	11	4	I52708	ELAV-like neuronal
43	2	18.2	11	4	S52252	hypothetical prote
44	1	9.1	11	1	XAVIBH	bradykinin-potenti
45	1	9.1	11	1	XASNBA	bradykinin-potenti
46	1	9.1	11	1	ECLQ2M	tachykinin II - mi
47	1	9.1	11	1	SPHO	substance P - hors
48	1	9.1	11	1	EOOCC	eledoisin - curled
49	1	9.1	11	1	A60654	substance P - guin
50	1	9.1	11	1	EOOC	eledoisin - musky
51	1	9.1	11	1	GMROL	leucosulfakinin -
52	1	9.1	11	1	LFTWWE	probable trpEG lea
53	1	9.1	11	2	S66196	alcohol dehydrogen
54	1	9.1	11	2	G42762	proteasome endopep
55	1	9.1	11	2	A33917	dihydroorotase (EC
56	1	9.1	11	2	B49164	chromogranin-B - r
57	1	9.1	11	2	JN0023	substance P - chic
58	1	9.1	11	2	PQ0682	photosystem I 17.5
59	1	9.1	11	2	S00616	parasporal crystal
60	1	9.1	11	2	C53652	rhlR protein - Pse
61	1	9.1	11	2	S09074	cytochrome P450-4b
62	1	9.1	11	2	A57458	gene Gax protein -
63	1	9.1	11	2	D60409	kassinin-like pept
64	1	9.1	11	2	F60409	substance P-like p
65	1	9.1	11	2	E60409	substance P-like p
66	1	9.1	11	2	YHRT	morphogenetic neur
67	1	9.1	11	2	YHHU	morphogenetic neur
68	1	9.1	11	2	YHBO	morphogenetic neur
69	1	9.1	11	2	YHXAE	morphogenetic neur
70	1	9.1	11	2	YHJFHY	morphogenetic neur

71	1	9.1	11	2	A61365	phyllokinin - Rohd
72	1	9.1	11	2	S23308	substance P - rain
73	1	9.1	11	2	S23306	substance P - Atla
74	1	9.1	11	2	B60409	kassinin-like pept
75	1	9.1	11	2	C60409	kassinin-like pept
76	1	9.1	11	2	S07203	uperolein - frog (
77	1	9.1	11	2	S07207	Crinia-angiotensin
78	1	9.1	11	2	S07201	physalaemin - frog
79	1	9.1	11	2	A61033	ranatachakinin A -
80	1	9.1	11	2	D61033	ranatachakinin D -
81	1	9.1	11	2	S42449	ant1 protein - pha
82	1	9.1	11	2	B58501	24K kidney and bla
83	1	9.1	11	2	D58502	27K bile and gallb
84	1	9.1	11	2	A58502	38K kidney stone p
85	1	9.1	11	2	C58501	42K bile stone pro
86	1	9.1	11	2	F58501	43.5K bile stone p
87	1	9.1	11	2	PQ0231	beta-glucosidase (
88	1	9.1	11	2	S04875	nifS protein - Bra
89	1	9.1	11	2	I41138	acetyl ornithine d
90	1	9.1	11	2	S42587	celF protein - Esc
91	1	9.1	11	2	S35490	type II site-speci
92	1	9.1	11	2	S21127	precorrin methyltr
93	1	9.1	11	2	S70720	trigger factor hom
94	1	9.1	11	2	S33782	acetolactate synth
95	1	9.1	11	2	B39853	LuxC protein - Pho
96	1	9.1	11	2	A58838	hemolysin - Porphy
97	1	9.1	11	2	B43669	hypothetical prote
98	1	9.1	11	2	D60691	phycobilisome 9K 1
99	1	9.1	11	2	PC2330	cycloinulooligosac
100	1	9.1	11	2	B41835	translation elonga

ALIGNMENTS

RESULT 1

PH0919

T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0919

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0919

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

A;Note: the authors translated the codon CAG for residue 11 as Glu

C;Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 3 SRD 5

RESULT 2
S32575
ribosomal protein S2, plastid - squawroot plastid (fragment)
C;Species: plastid Conopholis americana (squawroot)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
C;Accession: S32575
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of
photosynthesis in a lineage of parasitic plants.
A;Reference number: S32575; MUID:92145776; PMID:1723664
A;Accession: S32575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <TAY>
A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C;Genetics:
A;Gene: rps2
A;Genome: plastid
C;Superfamily: Escherichia coli ribosomal protein S2
C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
|||
Db 1 MT 2

RESULT 3
A40693
transgelin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997
C;Accession: A40693
R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.
J. Cell Biol. 121, 1065-1073, 1993
A;Title: Purification and properties of transgelin: a transformation and shape
change sensitive actin-gelling protein.
A;Reference number: A40693; MUID:93273790; PMID:8501116
A;Accession: A40693
A;Molecule type: protein
A;Residues: 1-11 <SHA>
A;Experimental source: aorta
C;Comment: This protein gels actin and is down regulated by transformation or
loss of cell adherence in culture.
C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth
muscle protein SM22 homology
C;Keywords: actin binding; cytoskeleton

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 4

A38841

rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)
N;Alternate names: visual pigment protein
C;Species: *Watasenia scintillans* (sparkling enope)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997
C;Accession: A38841
R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
Biochim. Biophys. Acta 957, 318-321, 1988
A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.
A;Reference number: PT0063; MUID:89051045; PMID:3191148
A;Accession: A38841
A;Molecule type: protein
A;Residues: 1-11 <SEI>
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; retinal
F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 6 AI 7

RESULT 5

A26930

ermG leader peptide 1 - *Bacillus sphaericus*
C;Species: *Bacillus sphaericus*
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999
C;Accession: A26930
R;Monod, M.; Mohan, S.; Dubnau, D.
J. Bacteriol. 169, 340-350, 1987
A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.
A;Reference number: A91840; MUID:87083389; PMID:3025178
A;Accession: A26930
A;Molecule type: DNA
A;Residues: 1-11 <MON>
A;Cross-references: GB:MI5332; NID:g142881; PIDN:AAA22417.1; PID:g142882
C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
||
Db 7 RD 8

RESULT 6

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 9 RK 10

RESULT 7

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>

A;Cross-references: GB:L18897

A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 10 AR 11

RESULT 8

S66606
quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66606
R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.
A;Reference number: S66606; MUID:96035889; PMID:7556204
A;Accession: S66606
A;Molecule type: protein
A;Residues: 1-11 <SCH>
A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4
||
Db 2 KS 3

RESULT 9

S58244
pyrroloquinoline quinone synthesis C - Pseudomonas fluorescens (fragment)
C;Species: Pseudomonas fluorescens
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C;Accession: S58244
R;Schnider, U.; Keel, C.; Defago, G.; Haas, D.
submitted to the EMBL Data Library, May 1995
A;Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens
CHA0: their involvement in the production of the antibiotic pyoluteorin.
A;Reference number: S58239
A;Accession: S58244
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <SCH>
A;Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60734.1; PID:g929806

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 10

E60691

phycobilisome 8K linker protein - Synechococcus sp. (PCC 7002) (fragment)
C;Species: Synechococcus sp.
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C;Accession: E60691
R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.
Arch. Microbiol. 153, 550-560, 1990
A;Title: Structural and compositional analyses of the phycobilisomes of
Synechococcus sp. PCC 7002. Analyses of the wild-type strain and a phycocyanin-
less mutant constructed by interposon mutagenesis.
A;Reference number: A60691; MUID:90314662; PMID:2164365
A;Accession: E60691
A;Molecule type: protein
A;Residues: 1-11 <BRY>
C;Comment: This protein, one of the eleven components detected in this species
of the phycobilisome that helps to trap light energy for photosystem II, does
not carry a chromophore.
C;Keywords: photosystem II

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 7 TA 8

RESULT 11

PC2372

58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4)
(fragment)
C;Species: Bacillus cereus
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PC2372
R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano,
S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of
sporulation in Bacillus cereus.
A;Reference number: PC2369; MUID:95218265; PMID:7766022
A;Accession: PC2372
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <MAS>
C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 10 AR 11

RESULT 12

A44755

20alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) - Clostridium scindens (fragment)

C;Species: Clostridium scindens

C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 17-Mar-1999

C;Accession: A44755

R;Krafft, A.E.; Hylemon, P.B.

J. Bacteriol. 171, 2925-2932, 1989

A;Title: Purification and characterization of a novel form of 20alpha-hydroxysteroid dehydrogenase from Clostridium scindens.

A;Reference number: A44755; MUID:89255043; PMID:2722736

A;Accession: A44755

A;Molecule type: protein

A;Residues: 1-11 <KRA>

C;Comment: This enzyme was purified to homogeneity and shown to have 20alpha hydroxysteroid dehydrogenase activity in the presence of NADH or NADPH. The enzyme as purified lacked glyceraldehyde-3-phosphate dehydrogenase (GAPDH) activity although the fragment shows near identity to known GAPDH sequences.

C;Keywords: homotetramer; NAD; NADP; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 5 AI 6

RESULT 13

S33519

probable secreted protein - Acholeplasma laidlawii (fragment)

C;Species: Acholeplasma laidlawii

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from Acholeplasma laidlawii which restore export of beta-lactamase in Escherichia coli.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 7 MT 8

RESULT 14

G61497

seed protein ws-23 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: G61497
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from
two-dimensional gel.
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: G61497
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HIR>
C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4
||
Db 2 KS 3

RESULT 15

PC4267

ribosomal protein L12.1 - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: PC4267
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A;Reference number: PC4267
A;Accession: PC4267
A;Molecule type: protein
A;Residues: 1-11 <KAW>
A;Experimental source: strain Japonica Nihonbare

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 2 TA 3

RESULT 16

A38590

transforming protein (Ddras) - slime mold (Dictyostelium discoideum) (fragment)

C;Species: Dictyostelium discoideum
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-Sep-1993
C;Accession: A38590

R;Esch, R.K.; Firtel, R.A.
Genes Dev. 5, 9-21, 1991

A;Title: cAMP and cell sorting control the spatial expression of a developmentally essential cell-type-specific ras gene in Dictyostelium.

A;Reference number: A38590; MUID:91115102; PMID:1703508

A;Accession: A38590

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <ESC>

A;Cross-references: GB:Z11804; GB:K02114; GB:X58190

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 17

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999

C;Accession: A34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.

A;Reference number: A34135

A;Accession: A34135

A;Molecule type: protein

A;Residues: 1-11 <TIT>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 8 RK 9

RESULT 18

A61512

variant surface glycoprotein MITat 1.7 - Trypanosoma brucei (fragment)

C;Species: Trypanosoma brucei

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A;Title: Glycopeptides from variant surface glycoproteins of *Trypanosoma brucei*.
C-terminal location of antigenically cross-reacting carbohydrate moieties.
A;Reference number: A61512; MUID:81172836; PMID:6163983
A;Accession: A61512
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HOL>
C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 2 TA 3

RESULT 19
S05002
corazonin - American cockroach
C;Species: *Periplaneta americana* (American cockroach)
C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Apr-1998
C;Accession: S05002
R;Veenstra, J.A.
FEBS Lett. 250, 231-234, 1989
A;Title: Isolation and structure of corazonin, a cardioactive peptide from the
american cockroach.
A;Reference number: S05002; MUID:89325572; PMID:2753132
A;Accession: S05002
A;Molecule type: protein
A;Residues: 1-11 <VEE>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 6 SR 7

RESULT 20
S65395
chemical-sense-related lipophilic-ligand-binding protein - fruit fly (*Drosophila melanogaster*) (fragment)
C;Species: *Drosophila melanogaster*
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S65395
R;Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.
Eur. J. Biochem. 230, 298-308, 1995

A;Title: A putative lipophilic stimulant carrier protein commonly found in the taste and olfactory systems. A unique member of the pheromone-binding protein superfamily.

A;Reference number: S65394; MUID:95324537; PMID:7601113

A;Accession: S65395

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <OZA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6

||

Db 6 RD 7

RESULT 21

E57789

gallbladder stone matrix protein, 25K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C;Accession: E57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: E57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3

||

Db 2 RK 3

RESULT 22

S21727

gamma-interferon-induced protein IP-30 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S21727

R;Wei, M.L.; Cresswell, P.

Nature 356, 443-446, 1992

A;Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-derived peptides.

A;Reference number: S21727; MUID:92212461; PMID:1557127

A;Accession: S21727

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <WEI>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 7 TA 8

RESULT 23

PT0249

Ig heavy chain CRD3 region (clone 2-109A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0249
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0249
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
||
Db 7 RD 8

RESULT 24

PT0273

Ig heavy chain CRD3 region (clone 3-109A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0273
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0273
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 2 SR 3

RESULT 25

S13279
Ile-Ser-bradykinin - human (fragment)
N;Alternate names: T-kinin
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 24-Jul-1998
C;Accession: S13279
R;Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.;
Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A;Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human
malignant effusions.
A;Reference number: S13279; MUID:91166748; PMID:2076202
A;Accession: S13279
A;Molecule type: protein
A;Residues: 1-11 <WUN>
C;Keywords: bradykinin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 2 SR 3

RESULT 26

S68637
acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68637
R;Boschetti, N.; Brodbeck, U.
FEBS Lett. 380, 133-136, 1996
A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of
a single glycosylated protein of 22 kDa.
A;Reference number: S68637; MUID:96181683; PMID:8603722
A;Accession: S68637
A;Molecule type: protein
A;Residues: 1-11 <BOS>
A;Experimental source: brain
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4
||
Db 4 KS 5

RESULT 27

S54347

tubulin beta chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999

C;Accession: S54347

R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glial cells.

A;Reference number: S54343; MUID:95194333; PMID:7887910

A;Accession: S54347

A;Molecule type: protein

A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10

||

Db 6 AI 7

RESULT 28

PH1632

Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1632

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1632

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2

||

Db 2 AR 3

RESULT 29

PH1600

Ig H chain V-D-J region (wild-type clone 310) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1600
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1600
A;Molecule type: DNA
A;Residues: 1-11 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 30
PH1583
Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1583
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1583
A;Molecule type: DNA
A;Residues: 1-11 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 31
PH1584
Ig H chain V-D-J region (wild-type clone 8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1584
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-
less mice using a novel quantitative limiting dilution polymerase chain reaction
method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1584

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 32

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not
restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 33

PT0214

T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0214

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not
restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0214

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 3 AR 4

RESULT 34

C38887

T-cell receptor gamma chain (5a.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: C38887

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: C38887

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
||
Db 6 RD 7

RESULT 35

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
||
Db 10 RD 11

RESULT 36

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0929
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0929
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 37

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0947
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0947
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered
from experimentally induced allergic encephalomyelitis
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 38

T12264

cytochrome-c oxidase (EC 1.9.3.1) chain I - Laudakia caucasia mitochondrion
(fragment)

C;Species: mitochondrion Laudakia caucasia

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001

C;Accession: T12264; T12267; T12270; T12273; T12276; T12279

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12264

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC1>

A;Cross-references: EMBL:AF028681; NID:g3641460; PIDN: AAC99596.1; PID:g3641463

A;Experimental source: specimen voucher CAS185010; California Academy of Sciences, San Francisco

A;Accession: T12267

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC2>

A;Cross-references: EMBL:AF028682; NID:g3641464; PIDN: AAC99599.1; PID:g3641467

A;Accession: T12270

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC3>

A;Cross-references: EMBL:AF028683; NID:g3641468; PIDN: AAC99602.1; PID:g3641471

A;Accession: T12273

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC4>

A;Cross-references: EMBL:AF028684; NID:g3641472; PIDN: AAC99605.1; PID:g3641475

A;Accession: T12276

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC5>

A;Cross-references: EMBL:AF028686; NID:g3641480; PIDN: AAC99611.1; PID:g3641483

A;Accession: T12279

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC6>

A;Cross-references: EMBL:AF028687; NID:g3641484; PIDN: AAC99614.1; PID:g3641487

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match

18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 39

T12253

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia erythrogaster* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia erythrogaster*

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001

C;Accession: T12253; T12257

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12253

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC1>

A;Cross-references: EMBL:AF028679; NID:g3641452; PIDN: AAC99590.1; PID:g3641455

A;Experimental source: specimen voucher CAS182954; California Academy of Sciences, San Francisco

A;Accession: T12257

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC2>

A;Cross-references: EMBL:AF028680; NID:g3641456; PIDN: AAC99593.1; PID:g3641459

A;Experimental source: specimen voucher CAS184400; California Academy of Sciences, San Francisco

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 40

T12244

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia lehmanni* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia lehmanni*

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001

C;Accession: T12244

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 118-131, 1998
A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.
A;Reference number: Z17470; MUID:98424476; PMID:9751922
A;Accession: T12244
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <MAC>
A;Cross-references: EMBL:AF028677; NID:g3641444; PID:g3641447; PIDN: AAC99584.1
A;Experimental source: specimen voucher CAS183009; California Academy of Sciences, San Francisco
C;Genetics:
A;Gene: COI
A;Genome: mitochondrion
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 41
T12248
cytochrome-c oxidase (EC 1.9.3.1) chain I - Laudakia microlepis mitochondrion (fragment)
C;Species: mitochondrion Laudakia microlepis
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001
C;Accession: T12248
R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 118-131, 1998
A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.
A;Reference number: Z17470; MUID:98424476; PMID:9751922
A;Accession: T12248
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <MAC>
A;Cross-references: EMBL:AF028678; NID:g3641448; PID:g3641451; PIDN: AAC99587.1
A;Experimental source: specimen voucher GNM. RE. ex.-P120; Goteborg Natural History Museum Reptilia Exotica, Goteborg, Sweden
C;Genetics:
A;Gene: COI
A;Genome: mitochondrion
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 42

I52708

ELAV-like neuronal protein 1, truncated splice form - human
N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu
antigen D; paraneoplastic encephalomyelitis antigen
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: I52708
R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic
encephalomyelitis antigen in human lung cancer cell lines.
A;Reference number: I52708; MUID:94349312; PMID:8069866
A;Accession: I52708
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-11 <SEK>
A;Cross-references: GB:S73887; NID:g688242; PIDN:AAD14142.1; PID:g4261842
C;Comment: This abnormal peptide is expressed. For the long splice form, see
PIR:I38726.
C;Genetics:
A;Gene: GDB:ELAVL4; HUD; PNEM
A;Cross-references: GDB:141875; OMIM:168360
A;Map position: 1p36-1p36
C;Keywords: alternative splicing

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 5 SR 6

RESULT 43

S52252

hypothetical protein pco 5'-region - Escherichia coli plasmid pRJ1004 (fragment)
C;Species: Escherichia coli
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: S70166; S52252
R;Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.
Mol. Microbiol. 17, 1153-1166, 1995
A;Title: Molecular genetics and transport analysis of the copper-resistance
determinant (pco) from Escherichia coli plasmid pRJ1004.
A;Reference number: S70159; MUID:96130847; PMID:8594334
A;Accession: S70166
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <BRO>
A;Cross-references: EMBL:X83541; NID:g619126; PIDN:CAA58524.1; PID:g619127

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

C;Genetics:

A;Genome: plasmid pRJ1004

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 6 TA 7

RESULT 44

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive;

bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 3 R 3

RESULT 45

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 6 R 6

RESULT 46
ECLQ2M
tachykinin II - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995
C;Accession: S08266
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990
A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.
A;Reference number: S08265; MUID:90184489; PMID:2311766
A;Accession: S08266
A;Molecule type: protein
A;Residues: 1-11 <SCH>
C;Superfamily: tachykinin
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;1/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 47
SPHO
substance P - horse
C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558

A;Molecule type: protein
A;Residues: 1-11 <STU>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 48

EOOCC
eleodoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eleodoisin, the active
endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 3 S 3

RESULT 49

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 50

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 3 S 3

RESULT 51

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 5 D 5

RESULT 52

LFTWWE
probable trpEG leader peptide - *Thermus aquaticus*
C;Species: *Thermus aquaticus*
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S03315
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8
trpE and trpG.
A;Reference number: S03315; MUID:89000781; PMID:2844259
A;Accession: S03315
A;Molecule type: DNA
A;Residues: 1-11 <SAT>
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262
A;Note: the source is designated as *Thermus thermophilus* HB8
C;Genetics:
A;Gene: trpL
C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 1 M 1

RESULT 53

S66196
alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus*
sp.) (fragment)
C;Species: *Gadus* sp. (cod)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C;Accession: S66196
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196
A;Molecule type: protein
A;Residues: 1-11 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8
|
Db 1 T 1

RESULT 54

G42762
proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003
C;Accession: G42762
R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992
A;Title: Identification and localization of a cysteinyl residue critical for the
trypsin-like catalytic activity of the proteasome.
A;Reference number: A42762; MUID:92378961; PMID:1510924
A;Accession: G42762
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <DIC>
A;Note: sequence extracted from NCBI backbone (NCBIP:112176)
C;Superfamily: multicatalytic endopeptidase complex chain C9
C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 1 M 1

RESULT 55

A33917
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
C;Accession: A33917
R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.;
Bergh, S.T.; Evans, D.R.
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989
A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase
domain and interdomain linker in the CAD multifunctional polypeptide and
properties of the isolated domain.
A;Reference number: A33917; MUID:89282776; PMID:2543974
A;Accession: A33917

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <SIM>
A;Cross-references: GB:M23652
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; *Bacillus* dihydroorotate homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; *trpG* homology
C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 11 R 11

RESULT 56

B49164
chromogranin-B - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: B49164
R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.
A;Reference number: A49164; MUID:92063871; PMID:1954895
A;Accession: B49164
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <NIE>
A;Note: sequence extracted from NCBI backbone (NCBIP:66370)
C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 3 S 3

RESULT 57

JN0023
substance P - chicken
C;Species: *Gallus gallus* (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C;Accession: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023
A;Molecule type: protein
A;Residues: 1-11 <CON>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 58

PQ0682
photosystem I 17.5K'D2 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0682
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and
psaL are all present in isoforms in Nicotiana spp.
A;Reference number: PQ0667; MUID:94105345; PMID:8278548
A;Accession: PQ0682
A;Molecule type: protein
A;Residues: 1-11 <OBO>
C;Superfamily: photosystem I chain II
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 59

S00616
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain
galleriae 11-67) (fragment)
N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C;Species: Bacillus thuringiensis
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996
C;Accession: S00616
R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A;Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two
delta-endotoxins differing strongly in primary structure and entomocidal
activity.
A;Reference number: S00615
A;Accession: S00616

A;Molecule type: protein
A;Residues: 1-11 <CHE>
C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 4 A 4

RESULT 60

C53652
rhlR protein - *Pseudomonas aeruginosa* (fragment)
C;Species: *Pseudomonas aeruginosa*
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
C;Accession: C53652
R;Ochsner, U.A.; Fiechter, A.; Reiser, J.
J. Biol. Chem. 269, 19787-19795, 1994
A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.
A;Reference number: A53652; MUID:94327521; PMID:8051059
A;Accession: C53652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <OCH>
A;Cross-references: GB:L28170
C;Superfamily: sdiA regulatory protein

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 1 M 1

RESULT 61

S09074
cytochrome P450-4b - rat (fragment)
N;Alternate names: cytochrome P450K-5
N;Contains: oxidoreductase (EC 1.1.1.1)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
C;Accession: S09074
R;Imaoka, S.; Terano, Y.; Funae, Y.
Arch. Biochem. Biophys. 278, 168-178, 1990
A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.
A;Reference number: S09072; MUID:90210577; PMID:2321956

A;Accession: S09074
A;Molecule type: protein
A;Residues: 1-11 <IMA>
C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8
|
Db 5 T 5

RESULT 62

A57458
gene Gax protein - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
C;Accession: A57458
R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.
Mol. Cell. Biol. 15, 4272-4281, 1995

A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.

A;Reference number: A57458; MUID:95349593; PMID:7623821

A;Accession: A57458

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S79168; NID:g1050991

C;Genetics:

A;Gene: Gax

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 10 R 10

RESULT 63

D60409

kassinin-like peptide K-III - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: D60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 11 M 11

RESULT 64
F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C;Accession: F60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: F60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 11 M 11

RESULT 65
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C;Accession: E60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.
Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: E60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 5 D 5

RESULT 66

YHRT

morphogenetic neuropeptide - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 6 S 6

RESULT 67

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 6 S 6

RESULT 68

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 6 S 6

RESULT 69

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches	1;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	4	S	4						
Db	6	S	6						

RESULT 70

YHJFHY

morphogenetic neuropeptide - *Hydra attenuata*

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match	9.1%	Score	1;	DB	2;	Length	11;		
Best Local Similarity	100.0%	Pred.	No.	2e+05;					
Matches	1;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

Qy	4	S	4						
Db	6	S	6						

RESULT 71

A61365

phyllokinin - Rohde's leaf frog

N;Alternate names: bradykinin-isoleucyl-tyrosine O-sulfate

C;Species: *Phylomedusa rohdei* (Rohde's leaf frog)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61365

R;Anastasi, A.; Bertaccini, G.; Erspamer, V.

Br. J. Pharmacol. 27, 479-485, 1966

A;Title: Pharmacological data on phyllokinin (bradykinin-isoleucyl-tyrosine O-sulphate) and bradykinin-isoleucyl-tyrosine.

A;Reference number: A61365; MUID:67179312; PMID:5970899
A;Accession: A61365
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: sulfoprotein
F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 72

S23308
substance P - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S23308
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neuropeptide-Y-related peptides from the brain of the cod and trout.
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23308
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 73

S23306
substance P - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S23306

R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23306
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 74
B60409
kassinin-like peptide K-I - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C;Accession: B60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: B60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Note: this peptide was also found in a deamidated form
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 5 D 5

RESULT 75

C60409

kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6

|

Db 5 D 5

Search completed: April 8, 2004, 15:49:29

Job time : 9.61538 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-22

Perfect score: 11

Sequence: 1 ARKS RD MTAIK 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	4	36.4	11	12	US-10-344-878-5	Sequence 5, Appli
2	4	36.4	11	12	US-10-344-878-6	Sequence 6, Appli
3	3	27.3	11	8	US-08-424-550B-550	Sequence 550, App
4	3	27.3	11	9	US-09-935-682-19	Sequence 19, Appl
5	3	27.3	11	9	US-09-935-682-56	Sequence 56, Appl
6	3	27.3	11	9	US-09-813-653-22	Sequence 22, Appl
7	3	27.3	11	9	US-09-817-661-19	Sequence 19, Appl
8	3	27.3	11	9	US-09-873-676-4	Sequence 4, Appli
9	3	27.3	11	9	US-09-810-873-2	Sequence 2, Appli
10	3	27.3	11	9	US-09-758-128-25	Sequence 25, Appl
11	3	27.3	11	9	US-09-758-128-28	Sequence 28, Appl
12	3	27.3	11	9	US-09-949-196-16	Sequence 16, Appl
13	3	27.3	11	9	US-09-071-838-212	Sequence 212, App
14	3	27.3	11	9	US-09-758-426-25	Sequence 25, Appl
15	3	27.3	11	9	US-09-758-426-28	Sequence 28, Appl
16	3	27.3	11	9	US-09-758-198-25	Sequence 25, Appl
17	3	27.3	11	9	US-09-758-198-28	Sequence 28, Appl
18	3	27.3	11	10	US-09-983-802-567	Sequence 567, App
19	3	27.3	11	10	US-09-882-291-44	Sequence 44, Appl
20	3	27.3	11	10	US-09-861-661-25	Sequence 25, Appl
21	3	27.3	11	10	US-09-861-661-28	Sequence 28, Appl
22	3	27.3	11	10	US-09-809-391-698	Sequence 698, App
23	3	27.3	11	10	US-09-775-052-3	Sequence 3, Appli
24	3	27.3	11	10	US-09-847-946A-126	Sequence 126, App
25	3	27.3	11	10	US-09-847-946A-127	Sequence 127, App
26	3	27.3	11	10	US-09-880-748-3177	Sequence 3177, Ap
27	3	27.3	11	10	US-09-876-904A-33	Sequence 33, Appl
28	3	27.3	11	10	US-09-876-904A-236	Sequence 236, App
29	3	27.3	11	10	US-09-876-904A-509	Sequence 509, App
30	3	27.3	11	10	US-09-972-656-6	Sequence 6, Appli
31	3	27.3	11	10	US-09-802-083-10	Sequence 10, Appl
32	3	27.3	11	10	US-09-882-171-698	Sequence 698, App
33	3	27.3	11	12	US-09-973-278-398	Sequence 398, App
34	3	27.3	11	12	US-10-362-527-63	Sequence 63, Appl
35	3	27.3	11	12	US-10-430-685-39	Sequence 39, Appl
36	3	27.3	11	12	US-10-398-616-4	Sequence 4, Appli
37	3	27.3	11	12	US-10-398-616-10	Sequence 10, Appl
38	3	27.3	11	12	US-09-912-609-27	Sequence 27, Appl
39	3	27.3	11	14	US-10-060-019-1	Sequence 1, Appli
40	3	27.3	11	14	US-10-211-069-56	Sequence 56, Appl
41	3	27.3	11	14	US-10-062-710-168	Sequence 168, App
42	3	27.3	11	14	US-10-229-915-21	Sequence 21, Appl
43	3	27.3	11	14	US-10-227-616-68	Sequence 68, Appl
44	3	27.3	11	14	US-10-211-088-202	Sequence 202, App
45	3	27.3	11	14	US-10-136-738-2	Sequence 2, Appli
46	3	27.3	11	14	US-10-213-512-212	Sequence 212, App
47	3	27.3	11	14	US-10-165-732A-10	Sequence 10, Appl
48	3	27.3	11	14	US-10-172-785-10	Sequence 10, Appl
49	3	27.3	11	14	US-10-322-210-4	Sequence 4, Appli
50	3	27.3	11	14	US-10-077-065-2	Sequence 2, Appli
51	3	27.3	11	14	US-10-304-443-4	Sequence 4, Appli
52	3	27.3	11	14	US-10-008-524A-171	Sequence 171, App
53	3	27.3	11	14	US-10-168-445-83	Sequence 83, Appl
54	3	27.3	11	14	US-10-405-339-13	Sequence 13, Appl
55	3	27.3	11	15	US-10-376-121A-56	Sequence 56, Appl
56	3	27.3	11	15	US-10-350-719-171	Sequence 171, App

57	3	27.3	11	15	US-10-378-173-136	Sequence 136, App
58	3	27.3	11	15	US-10-032-037B-5	Sequence 5, Appli
59	3	27.3	11	15	US-10-032-037B-118	Sequence 118, App
60	3	27.3	11	15	US-10-032-037B-131	Sequence 131, App
61	3	27.3	11	15	US-10-032-037B-133	Sequence 133, App
62	3	27.3	11	15	US-10-032-037B-139	Sequence 139, App
63	3	27.3	11	15	US-10-032-037B-161	Sequence 161, App
64	3	27.3	11	15	US-10-032-037B-202	Sequence 202, App
65	3	27.3	11	15	US-10-029-988B-5	Sequence 5, Appli
66	3	27.3	11	15	US-10-029-988B-118	Sequence 118, App
67	3	27.3	11	15	US-10-029-988B-131	Sequence 131, App
68	3	27.3	11	15	US-10-029-988B-133	Sequence 133, App
69	3	27.3	11	15	US-10-029-988B-139	Sequence 139, App
70	3	27.3	11	15	US-10-029-988B-161	Sequence 161, App
71	3	27.3	11	15	US-10-029-988B-202	Sequence 202, App
72	3	27.3	11	15	US-10-032-423A-5	Sequence 5, Appli
73	3	27.3	11	15	US-10-032-423A-118	Sequence 118, App
74	3	27.3	11	15	US-10-032-423A-131	Sequence 131, App
75	3	27.3	11	15	US-10-032-423A-133	Sequence 133, App
76	3	27.3	11	15	US-10-032-423A-139	Sequence 139, App
77	3	27.3	11	15	US-10-032-423A-161	Sequence 161, App
78	3	27.3	11	15	US-10-032-423A-202	Sequence 202, App
79	3	27.3	11	15	US-10-014-099F-30	Sequence 30, Appl
80	3	27.3	11	15	US-10-149-138-552	Sequence 552, App
81	3	27.3	11	15	US-10-149-138-620	Sequence 620, App
82	3	27.3	11	15	US-10-149-138-1270	Sequence 1270, Ap
83	3	27.3	11	15	US-10-350-367-36	Sequence 36, Appl
84	2	18.2	11	8	US-08-450-842-46	Sequence 46, Appl
85	2	18.2	11	8	US-08-996-470-2	Sequence 2, Appli
86	2	18.2	11	8	US-08-424-550B-192	Sequence 192, App
87	2	18.2	11	8	US-08-424-550B-523	Sequence 523, App
88	2	18.2	11	8	US-08-841-636A-28	Sequence 28, Appl
89	2	18.2	11	8	US-08-817-832B-10	Sequence 10, Appl
90	2	18.2	11	8	US-08-765-837-15	Sequence 15, Appl
91	2	18.2	11	8	US-08-344-824-24	Sequence 24, Appl
92	2	18.2	11	9	US-09-222-179-1	Sequence 1, Appli
93	2	18.2	11	9	US-09-045-620-1	Sequence 1, Appli
94	2	18.2	11	9	US-09-113-924-18	Sequence 18, Appl
95	2	18.2	11	9	US-09-113-924-22	Sequence 22, Appl
96	2	18.2	11	9	US-09-739-907-108	Sequence 108, App
97	2	18.2	11	9	US-09-826-210-4	Sequence 4, Appli
98	2	18.2	11	9	US-09-770-621-37	Sequence 37, Appl
99	2	18.2	11	9	US-09-802-077-14	Sequence 14, Appl
100	2	18.2	11	9	US-09-802-077-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-10-344-878-5

; Sequence 5, Application US/10344878
 ; Publication No. US20040053848A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Virginia Patent Foundation
 ; APPLICANT: Allis, C. David
 ; APPLICANT: Strahl, Brian D

; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino t
; OTHER INFORMATION: erminus having MeLys at the fifth amino acid position.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: METHYLATION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)..(11)
; OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to a
; OTHER INFORMATION: id in the production of the antibody
US-10-344-878-5

Query Match 36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
||||
Db 3 ARKS 6

RESULT 2
US-10-344-878-6
; Sequence 6, Application US/10344878
; Publication No. US20040053848A1
; GENERAL INFORMATION:
; APPLICANT: The University of Virginia Patent Foundation
; APPLICANT: Allis, C. David
; APPLICANT: Strahl, Brian D
; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino t
; OTHER INFORMATION: erminus having MeLys at the fifth amino acid position.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: METHYLATION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)..(11)
; OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to a
; OTHER INFORMATION: id in the production of the antibody
US-10-344-878-6

Query Match 36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4
||||
Db 3 ARKS 6

RESULT 3

US-08-424-550B-550

; Sequence 550, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-550

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
 |||
Db 2 AIK 4

RESULT 4
US-09-935-682-19
; Sequence 19, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified
Nucleotide or
; TITLE OF INVENTION: Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/257,525
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/FR00/00460
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-682-19

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DMT 8
|||
Db 6 DMT 8

RESULT 5

US-09-935-682-56

; Sequence 56, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified Nucleotide or
; TITLE OF INVENTION: Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/257,525
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/FR00/00460
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-935-682-56

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAI 10
|||
Db 9 TAI 11

RESULT 6

US-09-813-653-22

; Sequence 22, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CPI-10070
US-09-813-653-22

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 5 SRD 7

RESULT 7

US-09-817-661-19

; Sequence 19, Application US/09817661
; Patent No. US20020076692A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane
; APPLICANT: Holet, Thor
; TITLE OF INVENTION: Improvements to ribosome display
; FILE REFERENCE: 84633
; CURRENT APPLICATION NUMBER: US/09/817,661
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/193,802
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-661-19

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 8

US-09-873-676-4

; Sequence 4, Application US/09873676
; Patent No. US20020077289A1

; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods
of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic binding peptide
US-09-873-676-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 5 AIK 7

RESULT 9
US-09-810-873-2
; Sequence 2, Application US/09810873
; Patent No. US20020106383A1
; GENERAL INFORMATION:
; APPLICANT: Mandrell, David
; APPLICANT: Bates, Anna
; APPLICANT: Brandon, David
; TITLE OF INVENTION: Monoclonal Antibodies Against Campylobacter jejuni and
Campylobacter coli
; TITLE OF INVENTION: Outer Membrane Antigens
; FILE REFERENCE: Mandrell
; CURRENT APPLICATION NUMBER: US/09/810,873
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/277,599
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()...()
; OTHER INFORMATION: The undetermined amino acid may or may not exist

US-09-810-873-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 10

US-09-758-128-25

; Sequence 25, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187Alman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mouse

US-09-758-128-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 11

US-09-758-128-28

; Sequence 28, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187Alman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128

; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-28

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 12

US-09-949-196-16

; Sequence 16, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF
Cdc25A IN RESPONSE
; TITLE OF INVENTION: TO DNA DAMAGE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-949-196-16

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 13

US-09-071-838-212

; Sequence 212, Application US/09071838

; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-212

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
| | |
Db 2 RKS 4

RESULT 14
US-09-758-426-25
; Sequence 25, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:

; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116Alman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-426-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
 |||
Db 7 DMT 9

RESULT 15

US-09-758-426-28

; Sequence 28, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116Alman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-28

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 16

US-09-758-198-25

; Sequence 25, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mouse

US-09-758-198-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 17

US-09-758-198-28

; Sequence 28, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-28

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 18

US-09-983-802-567

; Sequence 567, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 567
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-567

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 19

US-09-882-291-44

; Sequence 44, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence

US-09-882-291-44

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3

|||

Db 2 ARK 4

RESULT 20

US-09-861-661-25

; Sequence 25, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus sp.

US-09-861-661-25

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 21
US-09-861-661-28
; Sequence 28, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-861-661-28

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 7 DMT 9

RESULT 22
US-09-809-391-698
; Sequence 698, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 698
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-809-391-698

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 4 AIK 6

RESULT 23

US-09-775-052-3

; Sequence 3, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human

US-09-775-052-3

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 24

US-09-847-946A-126

; Sequence 126, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-126

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 25

US-09-847-946A-127

; Sequence 127, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-127

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 26

US-09-880-748-3177

; Sequence 3177, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3177
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-880-748-3177

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8
|||
Db 3 DMT 5

RESULT 27

US-09-876-904A-33

; Sequence 33, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Polyma
virus
; OTHER INFORMATION: major capsid protein VP1
US-09-876-904A-33

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 4 RKS 6

RESULT 28
US-09-876-904A-236
; Sequence 236, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-236

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 7 ARK 9

RESULT 29

US-09-876-904A-509

; Sequence 509, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Ig/EBP-1 (immunoglobulin
; OTHER INFORMATION: gene enhancer-binding protein).
US-09-876-904A-509

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 3 KSR 5

RESULT 30

US-09-972-656-6

; Sequence 6, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-972-656-6

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 6 ARK 8

RESULT 31

US-09-802-083-10

; Sequence 10, Application US/09802083
; Publication No. US20030119075A1
; GENERAL INFORMATION:
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Lowe, David G.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced
; TITLE OF INVENTION: Anticoagulant Potency
; FILE REFERENCE: P1736R1
; CURRENT APPLICATION NUMBER: US/09/802,083
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-802-083-10

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 3 SRD 5

RESULT 32

US-09-882-171-698

; Sequence 698, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493

; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,872
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/056,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894

; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AIK 11
|||
Db 4 AIK 6

RESULT 33

US-09-973-278-398

; Sequence 398, Application US/09973278
; Publication No. US20040044191A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P2
; CURRENT APPLICATION NUMBER: US/09/973,278
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/239,899
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,932

; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,919
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; PRIOR APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/055,722
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; PRIOR APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 398
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-973-278-398

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 34

US-10-362-527-63

; Sequence 63, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-362-527-63

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 6 SRD 8

RESULT 35

US-10-430-685-39

; Sequence 39, Application US/10430685
; Publication No. US20040039543A1
; GENERAL INFORMATION:
; APPLICANT: KECK, Peter
; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
; FILE REFERENCE: 63040-010210
; CURRENT APPLICATION NUMBER: US/10/430,685
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/US01/44000
; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: 60/246,196
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-430-685-39

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 3 RKS 5

RESULT 36

US-10-398-616-4

; Sequence 4, Application US/10398616
; Publication No. US20040054143A1
; GENERAL INFORMATION:
; APPLICANT: Ark Therapeutics Ltd.
; TITLE OF INVENTION: VEGF Peptides and Their Use for Inhibiting Angiogenesis
; FILE REFERENCE: GJE-6525
; CURRENT APPLICATION NUMBER: US/10/398,616
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/GB01/04736
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-10-398-616-4

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 7 KSR 9

RESULT 37

US-10-398-616-10

; Sequence 10, Application US/10398616
; Publication No. US20040054143A1
; GENERAL INFORMATION:
; APPLICANT: Ark Therapeutics Ltd.
; TITLE OF INVENTION: VEGF Peptides and Their Use for Inhibiting Angiogenesis

; FILE REFERENCE: GJE-6525
; CURRENT APPLICATION NUMBER: US/10/398,616
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/GB01/04736
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-10-398-616-10

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 6 KSR 8

RESULT 38
US-09-912-609-27
; Sequence 27, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-27

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RDM 7

|||
Db 6 RDM 8

RESULT 39

US-10-060-019-1

; Sequence 1, Application US/10060019
; Publication No. US20030003564A1
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/10/060,019
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/177,165
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*

US-10-060-019-1

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10

|||

Db 4 TAI 6

RESULT 40

US-10-211-069-56

; Sequence 56, Application US/10211069
; Publication No. US20030021797A1
; GENERAL INFORMATION:
; APPLICANT: DATTA, Syamal K
; APPLICANT: KALIYAPERUMAL, Arunan
; TITLE OF INVENTION: LOCALIZATION OF MAJOR PEPTIDE AUTOEPITOPES FOR NUCLEOSOME
SPECIF
; TITLE OF INVENTION: IC T CELLS OF SYSTEMIC LUPUS ERYTHEMATOSUS
; FILE REFERENCE: 290-13U1 (53662-5017
; CURRENT APPLICATION NUMBER: US/10/211,069
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/561,490
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,448
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Histone fragment
US-10-211-069-56

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5
|||
Db 9 KSR 11

RESULT 41
US-10-062-710-168

; Sequence 168, Application US/10062710
; Publication No. US2003004925A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV B Cell Epitopes
US-10-062-710-168

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 5 SRD 7

RESULT 42
US-10-229-915-21
; Sequence 21, Application US/10229915
; Publication No. US20030083262A1

; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: PPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/316,328
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-21

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 43
US-10-227-616-68
; Sequence 68, Application US/10227616
; Publication No. US20030099662A1
; GENERAL INFORMATION:
; APPLICANT: Boyd, Robert Simon
; APPLICANT: Stamps, Alasdair Craig
; APPLICANT: Terrett, Jonathan Alexander
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 2543-1-028
; CURRENT APPLICATION NUMBER: US/10/227,616
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: GB 0004576.5
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: GB 0031341.1
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-227-616-68

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 9 AIK 11

RESULT 44
US-10-211-088-202
; Sequence 202, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For
Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-202

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 4 RKS 6

RESULT 45
US-10-136-738-2
; Sequence 2, Application US/10136738
; Publication No. US20030108886A1
; GENERAL INFORMATION:
; APPLICANT: Finn, John
; APPLICANT: MacLachlan, Ian
; APPLICANT: Protiva Biotherapeutics Inc.
; TITLE OF INVENTION: Autogene Nucleic Acids Encoding a
; TITLE OF INVENTION: Secretable RNA Polymerase
; FILE REFERENCE: 020801-000310US
; CURRENT APPLICATION NUMBER: US/10/136,738
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,974
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-Tat variant secretion domain
US-10-136-738-2

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 46

US-10-213-512-212

; Sequence 212, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.

US-10-213-512-212

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 2 RKS 4

RESULT 47

US-10-165-732A-10

; Sequence 10, Application US/10165732A
; Publication No. US20030124117A1
; GENERAL INFORMATION:
; APPLICANT: Refino, Canio J.
; APPLICANT: Bunting, Stuart
; APPLICANT: Kirchhofer, Daniel
; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND
ANTICOAGULANT AND/OR
; TITLE OF INVENTION: ANTIPLATELET AGENTS
; FILE REFERENCE: 11669.110USI1
; CURRENT APPLICATION NUMBER: US/10/165,732A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/802,083
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-165-732A-10

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 3 SRD 5

RESULT 48

US-10-172-785-10

; Sequence 10, Application US/10172785
; Publication No. US20030143225A1
; GENERAL INFORMATION:
; APPLICANT: Refino, Canio J.
; APPLICANT: Bunting, Stuart
; APPLICANT: Kirchhofer, Daniel
; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND
ANTICOAGULANT AND/OR
; TITLE OF INVENTION: ANTIPLATELET AGENTS
; FILE REFERENCE: 11669.110USI2
; CURRENT APPLICATION NUMBER: US/10/172,785
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/165,732
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 09/802,083
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-172-785-10

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 3 SRD 5

RESULT 49

US-10-322-210-4

; Sequence 4, Application US/10322210
; Publication No. US20030147906A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IgE, Antagonists
; TITLE OF INVENTION: Thereof, and Their Therapeutic Uses
; FILE REFERENCE: B45173
; CURRENT APPLICATION NUMBER: US/10/322,210
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/914,089
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904408.3
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9917144.9
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: GB 9918598.5
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918599.3
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918601.7
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918604.1
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918606.6
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9925618.2
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric

US-10-322-210-4

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 6 SRD 8

RESULT 50

US-10-077-065-2

; Sequence 2, Application US/10077065
; Publication No. US20030165501A1
; GENERAL INFORMATION:
; APPLICANT: DeAlmeida, Venita I., Stewart, Timothy A.
; TITLE OF INVENTION: TREATMENT INVOLVING DKK-1 OR ANTAGONISTS THEREOF
; FILE REFERENCE: P1872R1
; CURRENT APPLICATION NUMBER: US/10/077,065
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,435
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-077-065-2

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11
|||
Db 7 AIK 9

RESULT 51

US-10-304-443-4

; Sequence 4, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Human peptide sequence
US-10-304-443-4

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 6 SRD 8

RESULT 52

US-10-008-524A-171

; Sequence 171, Application US/10008524A
; Publication No. US20030175682A1
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
; TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 18396/1074
; CURRENT APPLICATION NUMBER: US/10/008,524A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 09/314,268
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn' Ver. 2.1
; SEQ ID NO 171
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-10-008-524A-171

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 53

US-10-168-445-83

; Sequence 83, Application US/10168445
; Publication No. US20030177518A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Anne E
; APPLICANT: Haralampidis, Kosmas
; APPLICANT: Bryan, Gregory T
; TITLE OF INVENTION: Plant Gene
; FILE REFERENCE: 0380-P02892US0
; CURRENT APPLICATION NUMBER: US/10/168,445
; CURRENT FILING DATE: 2002-10-30

; PRIOR APPLICATION NUMBER: PCT/GB00/04908
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: GB 9930394.3
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 0020217.6
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Avena strigosa
US-10-168-445-83

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 7 RKS 9

RESULT 54

US-10-405-339-13

; Sequence 13, Application US/10405339
; Publication No. US20030190364A1
; GENERAL INFORMATION:
; APPLICANT: Panitch, Alyssa
; APPLICANT: Seal, Brandon
; TITLE OF INVENTION: Biological Affinity Based Delivery Systems
; FILE REFERENCE: 9138-0079US
; CURRENT APPLICATION NUMBER: US/10/405,339
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/369,568
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-405-339-13

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 55

US-10-376-121A-56

; Sequence 56, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2) DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-376-121A-56

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9
 |||
Db 9 MTA 11

RESULT 56

US-10-350-719-171

; Sequence 171, Application US/10350719
; Publication No. US20030219726A1
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
; TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 18396/2162
; CURRENT APPLICATION NUMBER: US/10/350,719
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/GB01/01176
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: GB0018140.4
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-10-350-719-171

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 57

US-10-378-173-136

; Sequence 136, Application US/10378173
; Publication No. US20030232014A1
; GENERAL INFORMATION:
; APPLICANT: Burke et al.
; TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
; FILE REFERENCE: MDSP-P01-023
; CURRENT APPLICATION NUMBER: US/10/378,173
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/360787
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorylated peptide

; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: phosphorylation
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (4)..(4)
; OTHER INFORMATION: phosphorylation

US-10-378-173-136

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4
|||
Db 1 RKS 3

RESULT 58

US-10-032-037B-5

; Sequence 5, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-037B-5

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 59

US-10-032-037B-118

; Sequence 118, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 118
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-118

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 5 SRD 7

RESULT 60
US-10-032-037B-131
; Sequence 131, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-131

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 61

US-10-032-037B-133
; Sequence 133, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-133

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 62
US-10-032-037B-139
; Sequence 139, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-139

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6

|||
Db 2 SRD 4

RESULT 63
US-10-032-037B-161
; Sequence 161, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-161

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 64
US-10-032-037B-202
; Sequence 202, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-202

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 65

US-10-029-988B-5

; Sequence 5, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029, 988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258, 948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-029-988B-5

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 66

US-10-029-988B-118

; Sequence 118, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029, 988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258, 948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 118

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-118

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 5 SRD 7

RESULT 67

US-10-029-988B-131

; Sequence 131, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-131

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 68

US-10-029-988B-133

; Sequence 133, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-133

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 69

US-10-029-988B-139

; Sequence 139, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPEs CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPEs, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-139

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 70

US-10-029-988B-161

; Sequence 161, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-161

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 71
US-10-029-988B-202
; Sequence 202, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-202

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 72

US-10-032-423A-5

; Sequence 5, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-5

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 73

US-10-032-423A-118

; Sequence 118, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 118
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-118

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6

|||
Db 5 SRD 7

RESULT 74

US-10-032-423A-131

; Sequence 131, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-131

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 75

US-10-032-423A-133

; Sequence 133, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-133

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

Search completed: April 8, 2004, 16:35:50
Job time : 30.3077 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-22

Perfect score: 11

Sequence: 1 ARKS RDM TAIK 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

```
Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rat:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacterioplasm:*
17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result	Query							Description
No.	Score	Match	Length	DB	ID			

1	3	27.3	11	2	Q47602	Q47602 escherichia
2	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
3	2	18.2	11	2	Q47451	Q47451 escherichia
4	2	18.2	11	2	Q9AIZ7	Q9aiz7 carsonella
5	2	18.2	11	2	Q8RKN1	Q8rkn1 escherichia
6	2	18.2	11	2	Q8L2T4	Q8l2t4 neisseria m
7	2	18.2	11	2	P77404	P77404 escherichia
8	2	18.2	11	2	Q8RMI8	Q8rmi8 enterococcu
9	2	18.2	11	2	Q44090	Q44090 acholeplasm
10	2	18.2	11	2	Q44237	Q44237 anabaena sp
11	2	18.2	11	2	Q9R872	Q9r872 escherichia
12	2	18.2	11	2	Q8GL24	Q8gl24 borrelia bu
13	2	18.2	11	2	Q8GL19	Q8gl19 borrelia bu
14	2	18.2	11	2	Q7WUL8	Q7wul8 pseudomonas
15	2	18.2	11	3	Q9URG1	Q9urg1 neurospora
16	2	18.2	11	3	Q96V15	Q96v15 cryptococcu
17	2	18.2	11	4	Q14759	Q14759 homo sapien
18	2	18.2	11	4	Q9NY38	Q9ny38 homo sapien
19	2	18.2	11	4	Q9Y3G2	Q9y3g2 homo sapien
20	2	18.2	11	4	Q9UNL8	Q9unl8 homo sapien
21	2	18.2	11	4	Q9UCP5	Q9ucp5 homo sapien
22	2	18.2	11	4	Q16234	Q16234 homo sapien
23	2	18.2	11	4	Q9UBM2	Q9ubm2 homo sapien
24	2	18.2	11	4	Q8NI03	Q8ni03 homo sapien
25	2	18.2	11	4	Q9UCR1	Q9ucr1 homo sapien
26	2	18.2	11	4	Q9HCN5	Q9hcn5 homo sapien
27	2	18.2	11	5	Q25916	Q25916 plasmodium
28	2	18.2	11	5	Q9NFX0	Q9nfx0 drosophila
29	2	18.2	11	5	Q8MPQ3	Q8mpq3 caenorhabdi
30	2	18.2	11	6	Q9TRR7	Q9trr7 oryctolagus
31	2	18.2	11	6	Q9XSP7	Q9xsp7 pygathrix n
32	2	18.2	11	6	Q9XSP2	Q9xsp2 hylobates s
33	2	18.2	11	6	Q9XSP5	Q9xsp5 pan troglod
34	2	18.2	11	6	Q9TQS9	Q9tqs9 equus cabal
35	2	18.2	11	6	Q9TQS0	Q9tqs0 bos taurus
36	2	18.2	11	6	Q9XSP8	Q9xsp8 presbytis j
37	2	18.2	11	6	Q9XSP6	Q9xsp6 pongo pygma
38	2	18.2	11	6	Q9XSQ4	Q9xsq4 gorilla gor
39	2	18.2	11	7	077900	077900 oreochromis
40	2	18.2	11	7	077917	077917 oreochromis
41	2	18.2	11	7	077902	077902 oreochromis
42	2	18.2	11	7	077921	077921 pseudotroph
43	2	18.2	11	7	077901	077901 oreochromis
44	2	18.2	11	7	077916	077916 oreochromis
45	2	18.2	11	7	077905	077905 oreochromis
46	2	18.2	11	7	077899	077899 oreochromis
47	2	18.2	11	7	078121	078121 oreochromis
48	2	18.2	11	7	077904	077904 oreochromis
49	2	18.2	11	7	077903	077903 oreochromis
50	2	18.2	11	8	Q94V94	Q94v94 varanus sto
51	2	18.2	11	8	Q8ME62	Q8me62 porphyra ca
52	2	18.2	11	8	Q9G5W2	Q9g5w2 laudakia tu
53	2	18.2	11	8	Q9G622	Q9g622 salea horsf
54	2	18.2	11	8	Q94VG8	Q94vg8 varanus gou
55	2	18.2	11	8	Q9G5Y6	Q9g5y6 agama agama
56	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
57	2	18.2	11	8	Q9G5Y0	Q9g5y0 pseudotrape

58	2	18.2	11	8	Q9G5W5	Q9g5w5 laudakia nu
59	2	18.2	11	8	Q9G607	Q9g607 aphaniotis
60	2	18.2	11	8	Q94V77	Q94v77 heloderma s
61	2	18.2	11	8	Q79985	Q79985 laudakia ca
62	2	18.2	11	8	Q9G359	Q9g359 jalalura fl
63	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
64	2	18.2	11	8	Q9G649	Q9g649 otocryptis
65	2	18.2	11	8	Q9G643	Q9g643 calotes cal
66	2	18.2	11	8	Q9G5X4	Q9g5x4 trapelus ag
67	2	18.2	11	8	Q94V74	Q94v74 lanthanotus
68	2	18.2	11	8	Q8MESS5	Q8mess5 abelmoschus
69	2	18.2	11	8	Q9GD68	Q9gd68 elaeis guin
70	2	18.2	11	8	Q9G350	Q9g350 laudakia sa
71	2	18.2	11	8	Q8WD17	Q8wd17 ctenophorus
72	2	18.2	11	8	Q9G5Z8	Q9g5z8 acanthosaur
73	2	18.2	11	8	Q9G368	Q9g368 draco blanf
74	2	18.2	11	8	Q9G5W8	Q9g5w8 trapelus sa
75	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
76	2	18.2	11	8	Q94VE7	Q94ve7 varanus kom
77	2	18.2	11	8	Q94VB8	Q94vb8 varanus sal
78	2	18.2	11	8	Q9G353	Q9g353 trapelus sa
79	2	18.2	11	8	Q32704	Q32704 nicotiana t
80	2	18.2	11	8	Q79642	Q79642 laudakia mi
81	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
82	2	18.2	11	8	Q94VH7	Q94vh7 varanus gil
83	2	18.2	11	8	Q8SKR0	Q8skr0 rankinia di
84	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
85	2	18.2	11	8	Q9G619	Q9g619 ceratophora
86	2	18.2	11	8	Q8WER7	Q8wer7 ceratophora
87	2	18.2	11	8	Q8WD50	Q8wd50 ceratophora
88	2	18.2	11	8	Q94VK1	Q94vk1 varanus aca
89	2	18.2	11	8	Q9G356	Q9g356 agama atra
90	2	18.2	11	8	Q79639	Q79639 laudakia le
91	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
92	2	18.2	11	8	Q9G5V0	Q9g5v0 laudakia st
93	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
94	2	18.2	11	8	Q9G5X1	Q9g5x1 trapelus pe
95	2	18.2	11	8	Q8MERO	Q8mer0 hibiscus co
96	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
97	2	18.2	11	8	Q9G658	Q9g658 hydrosaurus
98	2	18.2	11	8	Q8ME54	Q8me54 porphyra um
99	2	18.2	11	8	Q8WER4	Q8wer4 ceratophora
100	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi

ALIGNMENTS

RESULT 1

Q47602

ID Q47602 PRELIMINARY; PRT; 11 AA.

AC Q47602;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE REase protein (Fragment).

GN REASE.

OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63620; AAA24558.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6
|||
Db 2 SRD 4

RESULT 2

Q9R790
ID Q9R790 PRELIMINARY; PRT; 11 AA.
AC Q9R790;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer surface protein C (Fragment).
GN OSPC.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G25;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "the Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93700; AAC45535.1; -.
DR GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.
DR GO:0003793; F:defense/immunity protein activity; IEA.
DR GO:0006952; P:defense response; IEA.
DR InterPro; IPR001800; Lipoprotein_6.
DR Pfam; PF01441; Lipoprotein_6; 1.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 8 AI 9

RESULT 3

Q47451

ID Q47451 PRELIMINARY; PRT; 11 AA.
AC Q47451;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Plasmid pRJ1004 DNA (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pRJ1004;
RX MEDLINE=96130847; PubMed=8594334;
RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;
RT "Molecular genetics and transport analysis of the copper-resistance
determinants (pco) from Escherichia coli plasmid pRJ1004.";
RL Mol. Microbiol. 17:1153-1166(1995).
DR EMBL; X83541; CAA58524.1; -.
DR PIR; S70166; S52252.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 6 TA 7

RESULT 4

Q9AIZ7

ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;

RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861 (2001).
DR EMBL; AF211132; AAK15377.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON TER 1 1
SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 6 IK 7

RESULT 5
Q8RKN1
ID Q8RKN1 PRELIMINARY; PRT; 11 AA.
AC Q8RKN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-lactamase CTX-M-9 (Fragment).
GN BLACTX-M-9.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=743-D;
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
RA Prats G.;
RT "A novel complex sul1-type integron in Escherichia coli carrying the
RT bla(CTX-M-9) gene.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY092058; AAM15718.1; -.
FT NON TER 1 1
SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 4 AR 5

RESULT 6

Q8L2T4

ID Q8L2T4 PRELIMINARY; PRT; 11 AA.
 AC Q8L2T4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Histidinol phosphatase (Fragment).
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=126E;
 RX MEDLINE=22051050; PubMed=12055303;
 RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;
 RT "Genetic Diversity of Three Lgt Loci for Biosynthesis of
 RT Lipooligosaccharide (LOS) in *Neisseria* Species.";
 RL *Microbiology* 148:1833-1844(2002).
 DR EMBL; AF470685; AAM33538.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1273 MW; 01EC828D0AA72050 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
 ||
 Db 8 RD 9

RESULT 7

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.
 AC P77404;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
 GN HSDR.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97206151; PubMed=9157244;
 RA Tyndall C., Lehnher H., Sandmeier U., Kulik E., Bickle T.A.;
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with
 RT high homology to the phage P1 genome: implications for the evolution
 RT and spread of DNA restriction systems.";
 RL *Mol. Microbiol.* 23:729-736(1997).
 DR EMBL; X98145; CAA66840.1; -.
 DR EMBL; X98144; CAA66839.1; -.

FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4
||
Db 1 KS 2

RESULT 8

Q8RMI8
ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
AC Q8RMI8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ErmB (Fragment).
GN ERMB.
OS Enterococcus hirae.
OG Plasmid pMKH1.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1354;
RN [1]
RP SEQUENCE FROM N.A.
RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
RT poultry origin.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF493942; AAM18554.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.

FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 10 RK 11

RESULT 9

Q44090
ID Q44090 PRELIMINARY; PRT; 11 AA.
AC Q44090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical export segment (Fragment).
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.

OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A-EF22;
RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
RT "Sequence regions from Acholeplasma laidlawii which restore export of
RT beta-lactamase in Escherichia coli.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z22875; CAA80495.1; -.
DR PIR; S33519; S33519.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 7 MT 8

RESULT 10
Q44237
ID Q44237 PRELIMINARY; PRT; 11 AA.
AC Q44237;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glutamine synthetase (Fragment).
GN GLNA.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;
RT "The apcF gene of Anabaena sp. strain PCC 7120 is regulated by
RT nitrogen and the apcF and glnA promoters overlap.";
RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA Scappino L.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U21853; AAA65652.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 11
Q9R872
ID Q9R872 PRELIMINARY; PRT; 11 AA.
AC Q9R872;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dihydrofolate reductase (Fragment).
GN DFR1.
OS Escherichia coli.
OG Plasmid r483.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn7;
RA Hansson K., Sundstrom L., Pelletier A., Roy P.H.;
RT "Sequence and function of the second type of integron in Tn7.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn7;
RX MEDLINE=82220022; PubMed=6283361;
RA Lichtenstein C., Brenner S.;
RT "Unique insertion site of Tn7 in the E. coli chromosome.";
RL Nature 297:601-603(1982).
RN [3]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn7;
RX MEDLINE=83290694; PubMed=6411680;
RA Simonsen C.C., Chen E.Y., Levinson A.D.;
RT "Identification of the type I trimethoprim-resistant dihydrofolate
RT reductase specified by the Escherichia coli R-plasmid R483: Comparison
RT with prokaryotic and eucaryotic dihydrofolate reductases.";
RL J. Bacteriol. 155:1001-1008(1983).
RN [4]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn7;
RX MEDLINE=83272957; PubMed=6308574;
RA Fling M.E., Richards C.;
RT "The nucleotide sequence of the trimethoprim-resistant dihydrofolate
RT reductase gene harbored by Tn7.";
RL Nucleic Acids Res. 11:5147-5158(1983).
DR EMBL; AJ001816; CAA05032.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

9 AI 10

||
Db 8 AI 9

RESULT 12

Q8GL24
ID Q8GL24 PRELIMINARY; PRT; 11 AA.
AC Q8GL24;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-6.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY142093; AAN17876.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1366 MW; 4E441D5330504373 CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 3 IK 4

RESULT 13

Q8GL19
ID Q8GL19 PRELIMINARY; PRT; 11 AA.
AC Q8GL19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-11.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32

RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY142096; AAN17880.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1366 MW; 4E441D5337204373 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 3 IK 4

RESULT 14
Q7WUL8
ID Q7WUL8 PRELIMINARY; PRT; 11 AA.
AC Q7WUL8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PdtJ (Fragment).
GN PDTJ.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3601;
RA Lewis T.A., Leach L., Morales S.E., Austin P.R., Hartwell H.J.,
RA Kaplan B., Forker C., Meyer J.-M.;
RT "Physiological and molecular genetic evaluation of the dechlorination
RT agent, pyridine-2,6-bis (monothiocarboxylic acid) (PDTC), as a
RT secondary siderophore of Pseudomonas sp.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY319946; AAQ01713.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1143 MW; C22A6E13A050587D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 3 TA 4

RESULT 15
Q9URG1
ID Q9URG1 PRELIMINARY; PRT; 11 AA.
AC Q9URG1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome C oxidase subunit 2 (Fragment).
OS *Neurospora crassa*.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; *Neurospora*.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92035058; PubMed=1657411;
RA Lemire E.G., Percy J.A., Correia J.M., Crowther B.M., Nargang F.E.;
RT "Alteration of the cytochrome c oxidase subunit 2 gene in the [exn-5]
RT mutant of *Neurospora crassa*.";
RL Curr. Genet. 20:121-127(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1222 MW; 936B1558C7605DC5 CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 5 AI 6

RESULT 16
Q96V15
ID Q96V15 PRELIMINARY; PRT; 11 AA.
AC Q96V15;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pheromone alpha (Fragment).
GN MFALPHA1A.
OS *Cryptococcus neoformans* var. *neoformans*.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IUM 98-3351;
RX MEDLINE=21538945; PubMed=11682503;
RA Cogliati M., Esposto M.C., Clarke D.L., Wickes B.L., Viviani M.A.;
RT "Origin of *Cryptococcus neoformans* var. *neoformans* Diploid Strains.";
RL J. Clin. Microbiol. 39:3889-3894(2001).
DR EMBL; AF377019; AAK55615.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1154 MW; C764AF6E786761ED CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8

||
Db 9 MT 10

RESULT 17

Q14759

ID Q14759 PRELIMINARY; PRT; 11 AA.
AC Q14759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lymphocyte cytosolic protein 2 (Fragment).
GN LCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sunden S.L.F., Carr L.L., Clements J.L., Motto D.G., Koretzky G.A.;
RT "Polymorphism in and localization of the gene encoding the 76 kDa SH2
RT domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-
RT qter.";
RL Genomics 0:0-0(1995).
DR EMBL; U44065; AAA93308.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DDD CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 7 RK 8

RESULT 18

Q9NY38

ID Q9NY38 PRELIMINARY; PRT; 11 AA.
AC Q9NY38;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Heavy metal-responsive transcription factor (Fragment).
GN MTF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA Georgiev O., Schaffner W.;
RT "Characterization of the mouse gene for the heavy metal-responsive
RT transcription factor MTF-1.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ251881; CAB71327.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 2 AI 3

RESULT 19
Q9Y3G2
ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.
AC Q9Y3G2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LSFR2 protein (Fragment).
GN LSFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299247; PubMed=10369878;
RA Gilley J., Fried M.;
RT "Extensive gene order differences within regions of conserved synteny
RT between the Fugu and human genomes: implications for chromosomal
RT evolution and the cloning of disease genes.";
RL Hum. Mol. Genet. 8:1313-1320(1999).
DR EMBL; Y17456; CAB44349.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 4 RK 5

RESULT 20
Q9UNL8
ID Q9UNL8 PRELIMINARY; PRT; 11 AA.
AC Q9UNL8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE APC2 protein (Fragment).
GN APC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,
RA Meredith D.M.;
RT "APC2 partial gene sequence.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF110338; AAD29275.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1326 MW; 75881D7BB441EAB4 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
||
Db 4 RD 5

RESULT 21
Q9UCP5
ID Q9UCP5 PRELIMINARY; PRT; 11 AA.
AC Q9UCP5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Aggrecan core protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92235266; PubMed=1569188;
RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;
RL J. Clin. Invest. 89:1512-1516(1992).
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR GO; GO:0001501; P:skeletal development; NAS.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1149 MW; 8FBFE8DFE72042D5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 1 AR 2

RESULT 22

Q16234

ID Q16234 PRELIMINARY; PRT; 11 AA.
AC Q16234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HuD protein (Fragment).
GN HUD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349312; PubMed=8069866;
RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;
RT "Molecular analysis of the HuD gene encoding a paraneoplastic
RT encephalomyelitis antigen in human lung cancer cell lines.";
RL Cancer Res. 54:4988-4992(1994).
DR EMBL; S73887; AAD14142.1; -.
DR PIR; I52708; I52708.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 5 SR 6

RESULT 23

Q9UBM2

ID Q9UBM2 PRELIMINARY; PRT; 11 AA.
AC Q9UBM2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ETV6 protein (Fragment).
GN ETV6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Montgomery K.T., Lau S.T., Renault B., Yoon S.J., Baens M.,
RA Marynen P., Kucherlapati R.;
RT "Towards the Complete Sequence of Chromosome 12.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Baens M., Peeters P., Guo C., Aerssens J., Marynen P.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U81830; AAB39862.1; --.
DR EMBL; U45432; AAB17016.1; --.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1194 MW; 8267C587A6DDC771 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 10 IK 11

RESULT 24
Q8NI03
ID Q8NI03 PRELIMINARY; PRT; 11 AA.
AC Q8NI03;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF500480; AAM21669.1; --.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 9 SR 10

RESULT 25
Q9UCR1
ID Q9UCR1 PRELIMINARY; PRT; 11 AA.
AC Q9UCR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 8 TA 9

RESULT 26
Q9HCN5
ID Q9HCN5 PRELIMINARY; PRT; 11 AA.
AC Q9HCN5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet glycoprotein VI (Fragment).
GN GPVI OR GP6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22359008; PubMed=12359731;
RA Holmes M.L., Bartle N., Eisbacher M., Chong B.H.;
RT "Cloning and Analysis of the Thrombopoietin-induced Megakaryocyte-
RT specific Glycoprotein VI Promoter and Its Regulation by GATA-1, Fli-1,
RT and Sp1.";
RL J. Biol. Chem. 277:48333-48341(2002).
DR EMBL; AB043943; BAB12248.1; -.
DR EMBL; AF521646; AAN86273.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1166 MW; 8D7839FE2DC1B775 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TA 9
||
Db 6 TA 7

RESULT 27

Q25916

ID Q25916 PRELIMINARY; PRT; 11 AA.
AC Q25916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Malaria antigen (7H8/2) (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91164876; PubMed=1706114;
RA Limpaiboon T., Taylor D., Jones G., Geysen H.M., Saul A.;
RT "Characterization of a Plasmodium falciparum epitope recognized by a
monoclonal antibody with broad isolate and species specificity.";
RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
DR EMBL; M31305; AAA29645.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 KS 4
||
Db 1 KS 2

RESULT 28

Q9NFX0

ID Q9NFX0 PRELIMINARY; PRT; 11 AA.
AC Q9NFX0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial aconitase (Fragment).
GN ACON OR MAC OR CG9244.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA Lind M.I.;
RT "Charaterisation of two iron regulatory proteins and mitochondrial

RT aconitase in *Drosophila melanogaster*.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ252019; CAB93522.1; -.
DR FlyBase; FBgn0010100; Acon.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 3 AR 4

RESULT 29
Q8MPQ3
ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.
AC Q8MPQ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Y23H5A.8b.
GN Y23H5A.8.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; *Caenorhabditis*.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode *C. elegans*: a platform for
RT investigating biology. The *C. elegans* Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Dempsey S., Le T.T.;
RT "The sequence of *C. elegans* cosmid Y23H5A.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF077541; AAM54173.1; -.
DR WormPep; Y23H5A.8b; CE31097.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 30

Q9TRR7

ID Q9TRR7 PRELIMINARY; PRT; 11 AA.
AC Q9TRR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein
DE L-13 fragment (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
RT "A calcyclin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 10 IK 11

RESULT 31

Q9XSP7

ID Q9XSP7 PRELIMINARY; PRT; 11 AA.
AC Q9XSP7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";

RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243282; CAB45924.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;
Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 32
Q9XSP2
ID Q9XSP2 PRELIMINARY; PRT; 11 AA.
AC Q9XSP2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243280; CAB45927.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;
Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 33
Q9XSP5
ID Q9XSP5 PRELIMINARY; PRT; 11 AA.
AC Q9XSP5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.

OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243277; CAB45926.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 34
Q9TQS9
ID Q9TQS9 PRELIMINARY; PRT; 11 AA.
AC Q9TQS9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Transferrin (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Giffard J.M., Brandon R.B., Bell T.K.;
RT "Further identification of single nucleotide polymorphisms in the
RT equine transferrin gene.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF185800; AAF05495.1; -.
DR EMBL; AF185797; AAF05492.1; -.
DR EMBL; AF185798; AAF05493.1; -.
DR EMBL; AF185799; AAF05494.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1231 MW; C586121E2DC4005D CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 4 AI 5

RESULT 35

Q9TQSO

ID Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene."
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ243424; CAB60775.1; -.
DR EMBL; AJ243060; CAB60774.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 1 IK 2

RESULT 36

Q9XSP8

ID Q9XSP8 PRELIMINARY; PRT; 11 AA.
AC Q9XSP8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Presbytis johnii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=98375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243281; CAB46013.1; -.
FT NON_TER 1 1

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 37

Q9XSP6

ID Q9XSP6 PRELIMINARY; PRT; 11 AA.
AC Q9XSP6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243279; CAB45925.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 3 SR 4

RESULT 38

Q9XSQ4

ID Q9XSQ4 PRELIMINARY; PRT; 11 AA.
AC Q9XSQ4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243278; CAB45916.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

 Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 SR 5
 ||
 Db 3 SR 4

RESULT 39
 077900
 ID 077900 PRELIMINARY; PRT; 11 AA.
 AC 077900;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050010; AAC41349.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 SR 5
 ||
 Db 8 SR 9

RESULT 40

077917

ID 077917 PRELIMINARY; PRT; 11 AA.
 AC 077917;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueiroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050030; AAC41369.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

 Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 SR 5
 ||
 Db 8 SR 9

RESULT 41

077902

ID 077902 PRELIMINARY; PRT; 11 AA.
 AC 077902;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueiroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";

RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050012; AAC41351.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

 Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 SR 5
 ||
 Db 8 SR 9

RESULT 42
 077921
 ID 077921 PRELIMINARY; PRT; 11 AA.
 AC 077921;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Pseudotropheus sp. 'Pseudotropheus tropheops complex'.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Pseudotropheus.
 OX NCBI_TaxID=51796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050034; AAC41373.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 SR 5
 ||
 Db 8 SR 9

RESULT 43
 077901
 ID 077901 PRELIMINARY; PRT; 11 AA.
 AC 077901;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueiroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050011; AAC41350.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 44
077916
ID 077916 PRELIMINARY; PRT; 11 AA.
AC 077916;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueiroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050029; AAC41368.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 45

077905

ID 077905 PRELIMINARY; PRT; 11 AA.
AC 077905;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050015; AAC41354.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 46

077899

ID 077899 PRELIMINARY; PRT; 11 AA.
AC 077899;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;

OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050009; AAC41348.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 47
078121
ID 078121 PRELIMINARY; PRT; 11 AA.
AC 078121;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050027; AAC41366.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1362 MW; 03C12D8EB7341B54 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||

Db 8 SR 9

RESULT 48
077904
ID 077904 PRELIMINARY; PRT; 11 AA.
AC 077904;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050014; AAC41353.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;
Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 49
077903
ID 077903 PRELIMINARY; PRT; 11 AA.
AC 077903;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050013; AAC41352.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 8 SR 9

RESULT 50
Q94V94
ID Q94V94 PRELIMINARY; PRT; 11 AA.
AC Q94V94;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus storri.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169855;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407531; AAL10145.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1387 MW; 8CBDEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 51
Q8ME62
ID Q8ME62 PRELIMINARY; PRT; 11 AA.
AC Q8ME62;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
(Fragment).
GN RBCL.
OS Porphyra carolinensis.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=76158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=75;
RA Teasdale B.W., West A., Taylor H., Klein A.S.;
RT "A Simple Restriction Fragment Length Polymorphism (RFLP) Assay To
RT Discriminate Common Porphyra (Rhodophyta) Taxa From The Northwest
RT Atlantic.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF414594; AAN03001.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1177 MW; D8DE49C4B771AB02 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9
||
Db 8 TA 9

RESULT 52
Q9G5W2
ID Q9G5W2 PRELIMINARY; PRT; 11 AA.
AC Q9G5W2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Laudakia tuberculata.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Laudakia.
OX NCBI_TaxID=118215;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;

RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128514; AAG00779.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 MT 8
 ||
 Db 4 MT 5

RESULT 53
 Q9G622
 ID Q9G622 PRELIMINARY; PRT; 11 AA.
 AC Q9G622;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Salea horsfieldii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Salea.
 OX NCBI_TaxID=118233;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128490; AAG00707.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

RESULT 54

Q94VG8

ID Q94VG8 PRELIMINARY; PRT; 11 AA.
AC Q94VG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus gouldii (Gould's monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62042;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407502; AAL10060.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 55

Q9G5Y6

ID Q9G5Y6 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Agama agama (Red-headed rock agama).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.
OX NCBI_TaxID=103336;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128504; AAG00749.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1324 MW; 9D52EC1E336415A1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 56
Q8MEL7
ID Q8MEL7 PRELIMINARY; PRT; 11 AA.
AC Q8MEL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Sida hookeriana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.
OX NCBI_TaxID=108446;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384624; AAM50396.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 6 RK 7

RESULT 57

Q9G5Y0
ID Q9G5Y0 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Pseudotrapelus sinaitus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Pseudotrapelus.
OX NCBI_TaxID=118229;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128507; AAG00758.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1374 MW; B05439FE336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 5 SR 6

RESULT 58

Q9G5W5
ID Q9G5W5 PRELIMINARY; PRT; 11 AA.

AC Q9G5W5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Laudakia nupta.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Laudakia.
 OX NCBI_TaxID=118212;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128513; AAG00776.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 MT 8
 ||
 Db 4 MT 5

RESULT 59
 Q9G607
 ID Q9G607 PRELIMINARY; PRT; 11 AA.
 AC Q9G607;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Aphaniotis fusca.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Aphaniotis.
 OX NCBI_TaxID=89036;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128495; AAG00722.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1389 MW; A68E371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 60
Q94V77
ID Q94V77 PRELIMINARY; PRT; 11 AA.
AC Q94V77;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Heloderma suspectum (Gila monster).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8554;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407540; AAL10172.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1396 MW; 8E3A6DE0D5A36411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 61

079985

ID 079985 PRELIMINARY; PRT; 11 AA.
AC 079985;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome C oxidase subunit I (Fragment).
GN COI.
OS Laudakia caucasia.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Laudakia.
OX NCBI_TaxID=71145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98424476; PubMed=9751922;
RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,
RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;
RT "Phylogenetic relationships among Agamid lizards of the Laudakia
RT caucasia species group: testing hypotheses of biogeographic
RT fragmentation and an area cladogram for the Iranian Plateau.";
RL Mol. Phylogen. Evol. 10:118-131(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20179532; PubMed=10712852;
RA Macey J.R., Schulte J.A. II, Kami H.G., Ananjeva N.B., Larson A.,
RA Papenfuss T.J.;
RT "Testing hypotheses of vicariance in the agamid lizard laudakia
RT caucasia from mountain ranges on the northern iranian plateau.";
RL Mol. Phylogen. Evol. 14:479-483(2000).
DR EMBL; AF028687; AAC99614.1; -.
DR EMBL; AF028681; AAC99596.1; -.
DR EMBL; AF028682; AAC99599.1; -.
DR EMBL; AF028683; AAC99602.1; -.
DR EMBL; AF028684; AAC99605.1; -.
DR EMBL; AF028685; AAC99608.1; -.
DR EMBL; AF028686; AAC99611.1; -.
DR EMBL; AF172705; AAF65208.1; -.
DR EMBL; AF172704; AAF65205.1; -.
DR PIR; T12264; T12264.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 62

Q9G359

ID Q9G359 PRELIMINARY; PRT; 11 AA.
AC Q9G359;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Japalura flaviceps.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Japalura.
OX NCBI_TaxID=52218;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128500; AAG00737.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1341 MW; 538E371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

RESULT 63

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
AC Q8MEM2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Lagunaria patersonia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
OX NCBI_TaxID=183274;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384616; AAM50388.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 6 RK 7

RESULT 64

Q9G649

ID Q9G649 PRELIMINARY; PRT; 11 AA.
AC Q9G649;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Otocryptis wiegmanni.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Otocryptis.
OX NCBI_TaxID=118220;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;

RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128480; AAG00677.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

RESULT 65
Q9G643
ID Q9G643 PRELIMINARY; PRT; 11 AA.
AC Q9G643;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes calotes.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).

DR EMBL; AF128482; AAG00683.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1373 MW; BE2D371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 66
Q9G5X4
ID Q9G5X4 PRELIMINARY; PRT; 11 AA.
AC Q9G5X4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Trapelus agilis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Trapelus.
OX NCBI_TaxID=52210;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128509; AAG00764.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1391 MW; BFC73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||

Db

4 MT 5

RESULT 67

Q94V74

ID Q94V74 PRELIMINARY; PRT; 11 AA.
AC Q94V74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Lanthanotus borneensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Lanthanotidae;
OC Lanthanotus.
OX NCBI_TaxID=62058;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407541; AAL10175.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1388 MW; 8F28EE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8

||

Db 1 MT 2

RESULT 68

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
AC Q8MES5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Abelmoschus manihot.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
OX NCBI_TaxID=183220;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using

RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL *Syst. Bot.* 27:333-350 (2002).
DR EMBL; AF384561; AAM50399.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 6 RK 7

RESULT 69

Q9GD68

ID Q9GD68 PRELIMINARY; PRT; 11 AA.
AC Q9GD68;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S16 (Fragment).
GN RPS16.
OS *Elaeis guineensis* var. *tenera* (Oil palm).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;
OC Coccoeae; Elaeidinae; Elaeis.
OX NCBI_TaxID=51953;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RAasmussen C.B., Chase M.W.;
RT "Coding and noncoding plastid DNA in palm systematics.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ404952; CAC17867.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1386 MW; 634693A666C2C044 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 1 AI 2

RESULT 70

Q9G350

ID Q9G350 PRELIMINARY; PRT; 11 AA.
 AC Q9G350;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Laudakia sacra.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Laudakia.
 OX NCBI_TaxID=52204;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128515; AAG00782.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;
 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
 ||
 Db 4 MT 5

RESULT 71
 Q8WD17
 ID Q8WD17 PRELIMINARY; PRT; 11 AA.
 AC Q8WD17;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Ctenophorus reticulatus (Western netted dragon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC Ctenophorus.
OX NCBI_TaxID=180002;
RN [1]
RP SEQUENCE FROM N.A.
RA Melville J., Schulte J.A. II, Larson A.;
RT "A molecular phylogenetic study of ecological diversification in the
RT Australian lizard genus Ctenophorus.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF375634; AAL40433.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1313 MW; A8F7371E336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 5 SR 6

RESULT 72
Q9G5Z8
ID Q9G5Z8 PRELIMINARY; PRT; 11 AA.
AC Q9G5Z8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Acanthosaura lepidogaster.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Acanthosaura.
OX NCBI_TaxID=118088;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128499; AAG00734.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1279 MW; 5DF7371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

RESULT 73
Q9G368
ID Q9G368 PRELIMINARY; PRT; 11 AA.
AC Q9G368;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Draco blanfordii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Draco.
OX NCBI_TaxID=89021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128477; AAG00668.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;
Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 5 SR 6

RESULT 74

Q9G5W8

ID Q9G5W8 PRELIMINARY; PRT; 11 AA.
AC Q9G5W8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS *Trapelus savignyi*.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC *Trapelus*.
OX NCBI_TaxID=118240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128512; AAG00773.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 4 MT 5

RESULT 75

Q8MEP0

ID Q8MEP0 PRELIMINARY; PRT; 11 AA.
AC Q8MEP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus peralbus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183256;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384598; AAM50370.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 6 RK 7

Search completed: April 8, 2004, 15:46:11
Job time : 28.7692 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
(without alignments)
111.135 Million cell updates/sec

Title: US-09-787-443A-22

Perfect score: 11

Sequence: 1 ARKS RDM TAIK 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3	27.3	11	1	UXB2_YEAST	P99013 saccharomy
2	2	18.2	11	1	BRK_MEGFL	P12797 megascolia
3	2	18.2	11	1	CORZ_PERAM	P11496 periplaneta
4	2	18.2	11	1	CSI5_BACSU	P81095 bacillus su
5	2	18.2	11	1	ES1_RAT	P56571 rattus norv
6	2	18.2	11	1	NUHM_CANFA	P49820 canis famil
7	2	18.2	11	1	NXSN_PSETE	P59072 pseudonaja
8	2	18.2	11	1	PQQC_PSEFL	P55173 pseudomonas
9	2	18.2	11	1	Q2OA_COMTE	P80464 comamonas t
10	2	18.2	11	1	RR2_CONAM	P42341 conopholis
11	2	18.2	11	1	RS30_ONCMY	P83328 oncorhynchus
12	2	18.2	11	1	TIN4_HOPTI	P82654 hoplobatrac
13	1	9.1	11	1	ANGT_CRIGE	P09037 crinia geor
14	1	9.1	11	1	ASL1_BACSE	P83146 bacteroides
15	1	9.1	11	1	ASL2_BACSE	P83147 bacteroides
16	1	9.1	11	1	BPP3_BOTIN	P30423 bothrops in
17	1	9.1	11	1	BPP4_BOTIN	P30424 bothrops in

18	1	9.1	11	1	BPPB_AGKHA	P01021 agkistrodon
19	1	9.1	11	1	BPP_AGKHP	P04562 agkistrodon
20	1	9.1	11	1	CA21_LITCI	P82087 litoria cit
21	1	9.1	11	1	CA22_LITCI	P82088 litoria cit
22	1	9.1	11	1	CA31_LITCI	P82089 litoria cit
23	1	9.1	11	1	CA32_LITCI	P82090 litoria cit
24	1	9.1	11	1	CA41_LITCI	P82091 litoria cit
25	1	9.1	11	1	CA42_LITCI	P82092 litoria cit
26	1	9.1	11	1	CEP1_ACHFU	P22790 achatina fu
27	1	9.1	11	1	COXA_CANFA	P99501 canis famil
28	1	9.1	11	1	CX5A_CONAL	P58848 conus aulic
29	1	9.1	11	1	CX5B_CONAL	P58849 conus aulic
30	1	9.1	11	1	CXL1_CONMR	P58807 conus marmo
31	1	9.1	11	1	EFG_CLOPA	P81350 clostridium
32	1	9.1	11	1	FAR6_PENMO	P83321 penaeus mon
33	1	9.1	11	1	FAR9_CALVO	P41864 calliphora
34	1	9.1	11	1	HS70_PINPS	P81672 pinus pinas
35	1	9.1	11	1	LADD_ONCMY	P81018 oncorhynchus
36	1	9.1	11	1	LPW_THETH	P05624 thermus the
37	1	9.1	11	1	LSK1_LEUMA	P04428 leucophaea
38	1	9.1	11	1	LSKP_PERAM	P36885 periplaneta
39	1	9.1	11	1	MHBI_KLEPN	P80580 klebsiella
40	1	9.1	11	1	MLG_THETS	P41989 theromyzon
41	1	9.1	11	1	MORN_HUMAN	P01163 homo sapien
42	1	9.1	11	1	OAIF_SARBU	P83518 sarcophaga
43	1	9.1	11	1	PKC1_CARMO	P82684 carausius m
44	1	9.1	11	1	PVK1_PERAM	P41837 periplaneta
45	1	9.1	11	1	RANC_RANPI	P08951 rana pipien
46	1	9.1	11	1	RE41_LITRU	P82074 litoria rub
47	1	9.1	11	1	RRPL_CHAV	P13179 chandipura
48	1	9.1	11	1	T2P1_PROVU	P31031 proteus vul
49	1	9.1	11	1	TIN1_HOPTI	P82651 hoplobatrachus
50	1	9.1	11	1	TKC2_CALVO	P41518 calliphora
51	1	9.1	11	1	TKN1_PSEGU	P42986 pseudophryne
52	1	9.1	11	1	TKN1_UPEIN	P82026 uperoleia i
53	1	9.1	11	1	TKN1_UPERU	P08612 uperoleia r
54	1	9.1	11	1	TKN2_PSEGU	P42987 pseudophryne
55	1	9.1	11	1	TKN2_UPERU	P08616 uperoleia r
56	1	9.1	11	1	TKN3_PSEGU	P42988 pseudophryne
57	1	9.1	11	1	TKN4_PSEGU	P42989 pseudophryne
58	1	9.1	11	1	TKN5_PSEGU	P42990 pseudophryne
59	1	9.1	11	1	TKNA_CHICK	P19850 gallus gallus
60	1	9.1	11	1	TKNA_GADMO	P28498 gadus morhua
61	1	9.1	11	1	TKNA_HORSE	P01290 equus caballus
62	1	9.1	11	1	TKNA_ONCMY	P28499 oncorhynchus
63	1	9.1	11	1	TKNA_RANCA	P22688 rana catesbeiana
64	1	9.1	11	1	TKNA_RANRI	P29207 rana ridibunda
65	1	9.1	11	1	TKNA_SCYCA	P41333 scyliorhinus
66	1	9.1	11	1	TKND_RANCA	P22691 rana catesbeiana
67	1	9.1	11	1	TKN_ELEMO	P01293 eleodone moschata
68	1	9.1	11	1	TKN_PHYFU	P08615 physalaemus
69	1	9.1	11	1	UF05_MOUSE	P38643 mus musculus
70	1	9.1	11	1	ULAG_HUMAN	P31933 homo sapiens

ALIGNMENTS

RESULT 1

UXB2_YEAST

ID UXB2_YEAST STANDARD; PRT; 11 AA.
 AC P99013;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=X2180-1A;
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
 RL Submitted (AUG-1995) to Swiss-Prot.
 CC -!-- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.20, its MW is: 9.2 kDa.
 DR SWISS-2DPAGE; P99013; YEAST.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
 |||
 Db 7 ARK 9

RESULT 2

BRK_MEGFL

ID BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 DE peptide ([Thr6]bradykinin)].
 OS *Megascolia flavifrons* (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scoliidae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp *Megascolia flavifrons*.";
 RL Toxicon 25:527-535(1987).
 RN [2]

RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuara T., Mantel P.;
RT "Two kinins isolated from the venom of *Megascolia flavifrons*.";
RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: Belongs to the bradykinin family.
DR PIR; B26744; B26744.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 9 RK 10

RESULT 3
CORZ_PERAM
ID CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from
the American cockroach.";
RL FEBS Lett. 250:231-234(1989).
CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
CC in the physiological regulation of the heart beat.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; S05002; S05002.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5
||
Db 6 SR 7

RESULT 4

CSI5_BACSU
ID CSI5_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC --!- SUBCELLULAR LOCATION: Cytoplasmic.
CC --!- INDUCTION: In response to low temperature.
CC --!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11
||
Db 4 IK 5

RESULT 5

ES1_RAT
ID ES1_RAT STANDARD; PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE ES1 protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -!- MISCELLANEOUS: By 2D-PAGE, the determined PI of this protein (spot
CC P2) is: 8.9, its MW is: 25 kDa.
CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 6
NUHM_CANFA
ID NUHM_CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC mitochondrial inner membrane.

CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro; IPR002023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6
||
Db 10 RD 11

RESULT 7
NXSN_PSETE
ID NXSN_PSETE STANDARD; PRT; 11 AA.
AC P59072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
OS Pseudonaja textilis (Eastern brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=8673;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99449602; PubMed=10518793;
RA Gong N.L., Armugam A., Jeyaseelan K.;
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
RT cloning, expression and protein characterization.";
RL Eur. J. Biochem. 265:982-989(1999).
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
CC acetylcholine receptors (nAChR).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
CC -!- SIMILARITY: Belongs to the snake toxin family.
DR InterPro; IPR003571; Snake_toxin.
DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT UNSURE 3 3
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RD 6
||
Db 8 RD 9

RESULT 8
PQQC_PSEFL
ID PQQC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
DE biosynthesis protein C) (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHA0;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqC family.
CC -----
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CC -----
DR EMBL; X87299; CAA60734.1; -.
DR PIR; S58244; S58244.
DR HAMAP; MF_00654; -; 1.
KW PQQ biosynthesis.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MT 8
||
Db 1 MT 2

RESULT 9

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.

AC P80464;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).

OS Comamonas testosteroni (Pseudomonas testosteroni).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae; Comamonas.

OX NCBI_TaxID=285;

RN [1]

RP SEQUENCE.

RC STRAIN=63;

RX MEDLINE=96035889; PubMed=7556204;

RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;

RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.";

RL Eur. J. Biochem. 232:536-544(1995).

CC -!- FUNCTION: Converts (3-methyl)-quinoline to (3-methyl)-2-oxo-1,2-dihydroquinoline.

CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-1(2H)-one + reduced acceptor.

CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.

CC -!- PATHWAY: Degradation of quinoline and (3-methyl)quinoline; first step.

CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and two gamma chains (Probable).

DR PIR; S66606; S66606.

KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4
 ||
 Db 2 KS 3

RESULT 10

RR2_CONAM

ID RR2_CONAM STANDARD; PRT; 11 AA.

AC P42341;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chloroplast 30S ribosomal protein S2 (Fragment).

GN RPS2.

OS Conopholis americana (Squawroot).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;

OC lamiids; Lamiales; Orobanchaceae; Orobanchaceae; Conopholis.

OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
RT of photosynthesis in a lineage of parasitic plants.";
RL Curr. Genet. 20:515-518(1991).
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8
||
Db 1 MT 2

RESULT 11
RS30_ONCMY
ID RS30_ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O., Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow

RT trout skin.";
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 7 AR 8

RESULT 12
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerinin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10
||
Db 5 AI 6

RESULT 13

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana.";
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 A 1
Db	1 A 1

RESULT 14

ASL1_BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
 AC P83146;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two

RT novel heparinases, from *Bacteroides stercoris* HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 I 10
|
Db 3 I 3

RESULT 15
ASL2_BACSE
ID ASL2_BACSE STANDARD; PRT; 11 AA.
AC P83147;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS *Bacteroides stercoris*.
OC Bacteria; Bacteroidetes; *Bacteroides* (class); Bacteroidales;
OC Bacteroidaceae; *Bacteroides*.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from *Bacteroides stercoris* HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8
|
Db 1 T 1

RESULT 16
BPP3_BOTIN
ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC --!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 6 R 6

RESULT 17
BPP4_BOTIN
ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 6 R 6

RESULT 18
BPPB_AGKHA
ID BPPB_AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 R 2
 |
 Db 6 R 6

RESULT 19
 BPP_AGKHP
 ID BPP_AGKHP STANDARD; PRT; 11 AA.
 AC P04562;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
 OS pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=86177022; PubMed=3008123;
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
 RT "Structure-function studies on the bradykinin potentiating peptide
 RT from Chinese snake venom (Agkistrodon halys pallas).";
 RL Peptides 6 Suppl. 3:339-342(1985).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; JC0002; XAVIBH.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 R 2
 |
 Db 3 R 3

RESULT 20

CA21_LITCI

ID CA21_LITCI STANDARD; PRT; 11 AA.

AC P82087;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 2.1/2.1Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodryadinae; Litoria.

OX NCBI_TaxID=94770;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=20057701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litoria citropa. Part 1. Sequence determination using electrospray mass spectrometry.";

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).

CC --!- FUNCTION: Hypotensive neuropeptide (Probable).

CC --!- SUBCELLULAR LOCATION: Secreted.

CC --!- TISSUE SPECIFICITY: Skin dorsal glands.

CC --!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being sulfated.

CC --!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.

CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE_NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 4 4 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6

Db 3 D 3

RESULT 21

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.

AC P82088;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 2.2/2.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC --!- FUNCTION: Hypotensive neuropeptide (Probable).
CC --!- SUBCELLULAR LOCATION: Secreted.
CC --!- TISSUE SPECIFICITY: Skin dorsal glands.
CC --!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
CC sulfated.
CC --!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 3 D 3

RESULT 22
CA31_LITCI
ID CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 D 6
 |
 Db 3 D 3

RESULT 23
 CA32_LITCI
 ID CA32_LITCI STANDARD; PRT; 11 AA.
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 3 D 3

RESULT 24
CA41_LITCI
ID CA41_LITCI STANDARD; PRT; 11 AA.
AC P82091;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.1/4.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -- FUNCTION: Hypotensive neuropeptide (Probable).
CC -- SUBCELLULAR LOCATION: Secreted.
CC -- TISSUE SPECIFICITY: Skin dorsal glands.
CC -- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
CC sulfated.
CC -- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
CC -- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 3 D 3

RESULT 25

CA42_LITCI

ID CA42_LITCI STANDARD; PRT; 11 AA.
AC P82092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.2/4.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 3 D 3

RESULT 26

CEP1_ACHFU

ID CEP1_ACHFU STANDARD; PRT; 11 AA.

AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica.";
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
 CC excitatory actions on the penis retractor muscle, the buccal
 CC muscle and the identified neurons controlling the buccal muscle
 CC movement of achatina.
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 DR PIR; A34662; A34662.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 S 4
 |
 Db 1 S 1

RESULT 27
 COXA_CANFA
 ID COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).

CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O₂ = 4 ferricyanochrome
CC c + 2 H₂O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
DR HSC-2DPAGE; P99501; DOG.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 S 4
|
Db 1 S 1

RESULT 28

CX5A_CONAL
ID CX5A CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; A59146; A59146.

KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 7 R 7

RESULT 29

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.
AC P58849;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5b.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC --!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice (By similarity).
CC --!- SUBCELLULAR LOCATION: Secreted.
CC --!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC --!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
CC --!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; B59146; B59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 7 R 7

RESULT 30
CXL1_CONMR
ID CXL1_CONMR STANDARD; PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=10988292;
RA Balaji R.A., Otake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RT venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522(2000).
CC -!-- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!-- SUBCELLULAR LOCATION: Secreted.
CC -!-- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!-- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -!-- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 6 K 6

RESULT 31
EFG_CLOPA
ID EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).

GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 32
FAR6_PENMO
ID FAR6_PENMO STANDARD; PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 D 6
|
Db 1 D 1

RESULT 33
FAR9_CALVO
ID FAR9_CALVO STANDARD PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 9.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; I41978; I41978.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
Db 5 K 5

RESULT 34

HS70_PINPS

ID HS70_PINPS STANDARD; PRT; 11 AA.

AC P81672;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Heat shock 70 kDa protein (Fragment).

OS Pinus pinaster (Maritime pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

OX NCBI_TaxID=71647;

RN [1]

RP SEQUENCE.

RC TISSUE=Needle;

RX MEDLINE=99274088; PubMed=10344291;

RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,

RA Frigerio J.-M., Plomion C.;

RT "Separation and characterization of needle and xylem maritime pine

RT proteins.";

RL Electrophoresis 20:1098-1108(1999).

CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein

CC (spot N164) is: 5.4, its MW is: 73 kDa.

CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

KW ATP-binding; Heat shock; Multigene family.

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 I 10

Db 3 I 3

RESULT 35

LADD_ONCMY

ID LADD_ONCMY STANDARD; PRT; 11 AA.

AC P81018;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Ladderlectin (Fragment).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.

RC TISSUE=Blood;

RX MEDLINE=97293418; PubMed=9149391;

RA Jensen L.E., Thiel S., Petersen T.E., Jenseunis J.C.;

RT "A rainbow trout lectin with multimeric structure.";

RL Comp. Biochem. Physiol. 116B:385-390(1997).

CC --!- FUNCTION: Lectin that binds sepharose.
CC --!- COFACTOR: Calcium is essential for sepharose binding.
CC --!- SUBUNIT: Multimeric.
KW Lectin; Calcium.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 36
LPW_THETH
ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC --!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7

Db 1 M 1

RESULT 37

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -!- FUNCTION: Change the frequency and amplitude of contractions of
CC the hingut. Inhibits muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
Db 5 D 5

RESULT 38

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
the American cockroach homologous to the leucosulfakinins.";
RL *Neuropeptides* 14:145-149(1989).
CC --!- FUNCTION: Stimulates hindgut contractions.
CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 4 D 4

RESULT 39
MHBI_KLEPN
ID MHBI_KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; PubMed=8760924;
RA Robson N.D., Parrott S., Cooper R.A.;
RT "In vitro formation of a catabolic plasmid carrying Klebsiella
RT pneumoniae DNA that allows growth of *Escherichia coli* K-12 on 3-
RT hydroxybenzoate.";
RL *Microbiology* 142:2115-2120(1996).
CC --!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
KW Isomerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 1 M 1

RESULT 40
MLG_THETS
ID MLG_THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Wattez C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum.";
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: Belongs to the POMC family.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 7 R 7

RESULT 41
MORN_HUMAN
ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;

RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,
 RT from coelenterates to humans.";
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantissima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 RT hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
 RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
 CC in the G2/mitosis transition.
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
 CC and was called head activator by the authors, because it induced
 CC head-specific growth and differentiation in this animal. It has
 CC been found in mammalian intestine and hypothalamus.
 DR PIR; A01427; YHRT.
 DR PIR; A93900; YHXAE.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJFHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
 |
 Db 6 S 6

RESULT 42
 OAIF_SARBU
 ID OAIF_SARBU STANDARD; PRT; 11 AA.
 AC P83518;

DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
DE ODAIF(1-9); Neb-ODAIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=22272747; PubMed=12383874;
RA Vandingen A., Hens K., Baggerman G., Macours N., Schoofs L.,
RA De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme
RT substrate from vitellogenetic ovaries of Neobellieria bullata.";
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
CC vitro.
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
CC terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
FT PEPTIDE 1 11 NEB-ODAIF.
FT PEPTIDE 1 9 NEB-ODAIF(1-9).
FT PEPTIDE 1 7 NEB-ODAIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
Db 2 K 2

RESULT 43
PKC1_CARMO
ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Predel R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick

RT insect, *Carausius morosus* (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 1 D 1

RESULT 44
PVK1_PERAM
ID PVK1_PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisynthetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT perisynthetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 45
RANC_RANPI
ID RANC_RANPI STANDARD; PRT; 11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8
|
Db 2 T 2

RESULT 46
RE41_LITRU
ID RE41_LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,

RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 4 D 4

RESULT 47
RRPL_CHAV
ID RRPL_CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299473; PubMed=2741347;
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RABDOVIRUSES AND
CC PARAMYXOVIRUSES.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL; J04350; AAA42917.1; -.

KW Transferase; RNA-directed RNA polymerase.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 1 M 1

RESULT 48

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.

AC P31031;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
(R.PvuI) (Fragment).

GN PVUIR.

OS Proteus vulgaris.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Proteus.

OX NCBI_TaxID=585;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 13315;

RX MEDLINE=93087186; PubMed=1454536;

RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;

RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system.";

RL Nucleic Acids Res. 20:5743-5747(1992).

CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.

CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC

DR EMBL; L04163; AAA25660.1; -.

DR PIR; S35490; S35490.

DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 I 10
|
Db 1 I 1

RESULT 49
TIN1_HOPTI
ID TIN1_HOPTI STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tigerinin-1.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 9 R 9

RESULT 50
TKC2_CALVO

ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

RESULT 51
TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";

RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B60409; B60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 D 6
 |
 Db 5 D 5

RESULT 52
 TKN1_UPEIN
 ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.

CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 53
TKN1_UPERU
ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Endean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 3 D 3

RESULT 54

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; C60409; C60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|

Db

5 D 5

RESULT 55

TKN2_UPERU

ID TKN2_UPERU STANDARD; PRT; 11 AA.
AC P08616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and bombesin-like peptides in the skin of the
RT Australian leptodactylid frog Uperoleia rugosa.";
RL Chem. Pharm. Bull. 28:689-695(1980).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 A 1

|

Db

2 A 2

RESULT 56

TKN3_PSEGU

ID TKN3_PSEGU STANDARD; PRT; 11 AA.
AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).

OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D60409; D60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7
|
Db 11 M 11

RESULT 57
TKN4_PSEGU
ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.

RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog *Pseudophryne guntheri*.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6
|
Db 5 D 5

RESULT 58
TKN5_PSEGU
ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS *Pseudophryne guentheri* (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; *Pseudophryne*.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog *Pseudophryne guntheri*.";
RL Peptides 11:299-304(1990).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; F60409; F60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 M 7
 |
 Db 11 M 11

RESULT 59
 TKNA_CHICK
 ID TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 60
TKNA_GADMO
ID TKNA_GADMO STANDARD PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23306; S23306.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|

Db 1 K 1

RESULT 61

TKNA_HORSE

ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Equus caballus (Horse), and
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN [1]
RP SEQUENCE.
RC SPECIES=Horse;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.porcellus;
RX MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 62

TKNA_ONCMY

ID TKNA_ONCMY STANDARD; PRT; 11 AA.

AC P28499;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P.

OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;

RT "Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.";

RL Eur. J. Biochem. 206:659-664(1992).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S23308; S23308.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).

SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 63

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.

AC P22688;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ranatachtykinin A (RTK A).

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A61033; A61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3 K 3
Db	1 K 1

RESULT 64
 TKNA_RANRI
 ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;

RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog *Rana ridibunda*.";
RL *J. Neurochem.* 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 65
TKNA_SCYCA
ID TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS *Scyliorhinus canicula* (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; *Scyliorhinus*.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, *Scyliorhinus canicula*.";
RL *Eur. J. Biochem.* 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.

DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 66
TKND_RANCA
ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin D (RTK D).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D61033; D61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 67

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
AC P01293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Eledoisin.
OS Eledone moschata (Musky octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eledoisin, the active
endecapeptide of the posterior salivary glands of Eledone.";
RL Arch. Biochem. Biophys. 101:56-65(1963).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01561; E0OC.
DR PIR; B01561; E0OCC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4
|
Db 3 S 3

RESULT 68

TKN_PHYFU

ID TKN_PHYFU STANDARD; PRT; 11 AA.

AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main
 active polypeptide of the skin of Physalaemus fuscumaculatus.";
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 A 1
 |
 Db 2 A 2

RESULT 69
 UF05_MOUSE
 ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P38643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!-- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 48 kDa.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 70

ULAG_HUMAN

ID ULAG_HUMAN STANDARD; PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!-- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 34 kDa.
DR SWISS-2DPAGE; P31933; HUMAN.
DR Siena-2DPAGE; P31933; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

Search completed: April 8, 2004, 15:47:24
Job time : 5.15385 secs